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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /ggn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /ggn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /ggn2_6/ptodata/1/iaa/RE_COMB.pep:*

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US-08-632-446-26
US-08-652-446-26
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sequence
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Search. History

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APPLICANT: Kapeller, Rosana
ITILE OF INVENTION: NOVEL MOLECULES OF THE HXI
ITILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo Bapiens
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GENERAL INFORMATION:
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Best Local Similarity
Matches 313; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5871960 5837487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS: ADDRESSE: PRETTY, SCHROEDER & POPLAWSKI STREET: 444 South Flower St. - Suite 1900
                                                                                                                                                                                                    STREET: 444 South |
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
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                                         US/08/463,081B
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; MOLECULE TYPE: peptide
US-08-463-081B-26
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US-08-461-379A-26
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                                                                                                                                                                                                                                    Sequence 26, Application US/08461379A
PATENT NO. 5871961
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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Best Local Similarity 99.4%;
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
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ETILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796
ETILING DATE: 20-NOV-91
ATTORNEY AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 96:
TELECOMMUNICATION INFORMATION:
TELECHHONE: (213) 622-7700
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
SOFTWARE: Version #1.25
                                                                                                                                    ADDRESSEE: Ratner & Prestia
ADDRESSEE: (B) STI
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
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STRANDEDNESS: n.a.
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                                                                                                                                                                                                 STREET:One Westlakes-Berwyn
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Pred. No. 1.6e-159;
0; Mismatches 2;
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US-08-462-390B-26
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REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEPAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        Sequence 26, Application US/08462390B
Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Ve
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STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
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APPLICATION NUMBER: & 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
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FILING DATE: 5-JUNE-
PRIOR APPLICATION DATA:
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                                                                                                                          STATE: E
                                                                                                                                           CITY: Valley Forge
STATE: Pennsylvania
                                                                                                                                                                               ADDRESSEE:
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Pred. No. 1.6e-159;
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                       Version
                         #1.25
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US-08-463-074B-26
; Sequence 26, Application US/08463074B
; Patent No. 6020155
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR1
; NUMBER OF SEQUENCES: 35
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICATION NUMBER: US
FILING DATE: 5-JUNE-19
PRIOR APPLICATION DATA:
                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DAF
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
                                                                           CITY: Los Angeles
STATE: California
                                                           COUNTRY:
                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 10-AUG APPLICATION NUMBER:
                                                                                                                       ADDRESSEE:
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(610)407-0701
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                                                                                                                      PRETTY,
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                                                                                                                       SCHROEDER & POPLAWSKI
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                                                                                                                                                                   Fusion
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: V1/10ana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE (213) 489-4210
INFORMATION FOR SEG ID NO: 26:
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MOLECULE TYPE: peptide
US-08-463-074B-26
                                                                                                                                                                                                       Sequence 26, Application US/08465585C Patent No. 6027914
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                      APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 313 amino acids
CITY: Los Angeles
STATE: Californiaa
COUNTRY: USA
ZIP: 900071
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                                                                         ADDRESSEE:
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                                                                                          PRETTY, SCHROEDER & POPLAWSKI
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Pred. No. 1.6e-159;
0; Mismatches 2;
                                                                             STREET
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ADDRESSEE:

PRETTY, SCHROEDER & POPLAWSKI
. (B) STREET:

444

South Flower St.

Suite 1900

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Sequence 26, Application US/08652446

Patent No. 6057427

GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRS
TITLE OF INVENTION: Delypeptide, Vector and Transformed Cell Thereof,
TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSE: PRETTY, SCHROEDER & POPLAMSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 311; Conservative
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Best Local Similarity
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/330,108

FILING DATE: 27-OCT-1994

APPLICATION NUMBER: USSN 08/104,736

FILING DATE: 10-AUG-1993

APPLICATION NUMBER: USSN 07/796,066

FILING DATE: 20-NOV-1991

ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Viviana Amzel, Ph. D.
REGISTATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
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Pred. No. 1.6e-159;
0; Mismatches 2;
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILLING DATE: 5-7UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILLING DATE: 5-7UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
APPLICATION NUMBER: 08/739,523
APPLICATION NUMBER: 08/739,523
                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/46
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: PPG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5.-UUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: 08/463,074
APPLICATION NUMBER: 08/463,074
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APPLICATION NUMBER: US
FILING DATE:
PRIOR APPLICATION DATA:
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STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: n.a
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         121
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                                                                                                                                              1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD
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      ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
                      ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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California
                                                                                                                                                                                                                                                                                                                  peptide
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5-JAN-1998
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Pred. No. 1.6e-159;
0; Mismatches 2;
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                                                                                                                                                                                         Gaps
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US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: MOVEL MOLECULES OF THE
; TITLE OF INVENTION: AND USE THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
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US-09-237-543-8
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; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HX
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 199-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; SEQ ID NO 8
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; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8
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Best Local Similarity 97.1
Matches 304; Conservative
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97.1%;
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Pred. No. 2.1e-157;
6; Mismatches 3;
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THE HKID-1-RELATED PROTEIN FAMILY

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APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF TH
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543
CURRENT FILING DATE: 199-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 7
SEQ ID NO 7
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US-09-237-543-7
; Sequence 7, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-237-543-7
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Best Local Similarity 93.9
Matches 294; Conservative
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Best Local Similarity 97.1
Matches 304; Conservative
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ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                               ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG
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97.1%;
                                                                                                                                                                                                                                 94.7%; Score 1582; DB 2;
93.9%; Pred. No. 6.2e-152;
tive 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/237,543A
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Pred. No. 2.1e-157;
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                                                                                                                                                                                                                                                                Length 313;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KAPELIEY, ROSANA
TITLE OF INVENTION: NOVEL MOLECULES OF THE
FITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-09-644-450-7
                                          Sequence 41, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded St.
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
Correspondence Steven A. Benner
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US-09-644-450-7
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Best Local Similarity
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
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                                                                                                                                                                                                                                                                                                                                                                                                EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.7%; Score 1582; DB 2; ilarity 93.9%; Pred. No. 6.2e-152; Conservative 10; Mismatches 9;
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                                                                                                     Structures
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RESULT 14
US-09-237-543-2
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; DATE: 1988
US-07-857-224B-41
               GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
                                                                                                    Sequence 2, Application Patent No. 6143540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 242; Conserv
   CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: none INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILIMS CO. 436
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (International) 41 1 632 2830
TELECOMMUNICATION (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: Protein kinase PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple MacIntosh 7.0 OPERATING SYSTEM: MacIntosh 7.0 SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,22 FILING DATE: 03/25/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
DESCRIPTION:
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LENGTH: 257
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
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ZATURE: Protein kinase;
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VOLUME: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
ZIP: (not
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TOPOLOGY: linear
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nilarity 94.2%;
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US/09/237,543A
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Pred. No. 4.1e-123;
9; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF TH.
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
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SEQ ID NO 2
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
US-09-644-450-2
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US-09-644-450-2
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 326
                                                                                                                                                                                        Query Match 67.8%; Score 1133; DB 2; Best Local Similarity 69.3%; Pred. No. 2.1e-106; Matches 219; Conservative 35; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09644450 Patent No. 6383791
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ORGANISM: Homo
               116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLBAVRHCHNCGVLHRDIKDENILI 175
119
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                                                                             VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
                                                                                                                           MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR
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FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV
                                                            TADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG
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Pred. No. 2.1e-106;
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Search Job ti	В	ঠ	В	8	Дb	ઠ
Search completed: May 4, 2006, 05:27:21 Job time : 29.6667 secs	299 GAP-ESCDLRLCTLDP 313	294 LLPQETAEIHLHSLSP 309	239 VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG 298	236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDV 293	179 DLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238	176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235

Run

protein -

54275, Appli 54275, Appli 166, Appli 166, Appli 166, Appli 167, Appli 17, Appli 17, Appli 17, Appli 18, Appli 19, Appli 19, Appli 10, Appli 11, Appli

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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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1: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptcdata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptcdata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptcdata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptcdata/1/pubpaa/US11_PUBCOMB.pep:*
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US-10-081-119-18
US-10-394-322A-52
US-10-348-081-13
US-10-664-421-150
US-10-705-757-2
US-10-951-406-18
US-10-951-406-18
US-10-951-477-18
US-10-951-477-18
US-10-971-635-152
US-10-941-635-152
US-10-941-635-152
US-09-971-791-8
US-10-348-081-12
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Patent No. US20020115120A1
GENERAL INFORMATION:
APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Laura A. Rudolph-Owen
APPLICANT: Kyle MacBeth
TITLE OF INVENTION: NOVEL MOLECULES OF THE H
TITLE OF INVENTION: NOVEL MOLECULES OF THE H
TILE REFERENCE: 35800/238856
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US/09/971,791
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
IENCTU. 13
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; TYPE: PRT
; ORGANISM: Homo s
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EIHLHSLSPGPSK 313
                                                                                             PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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US-09-971-791-2
US-10-644-421-166
US-10-664-421-166
US-10-18-941-82
US-10-425-114-54264
US-10-348-081-6
US-10-348-081-10
US-10-348-081-10
US-10-348-081-10
US-10-348-081-10
US-10-348-081-10
US-10-364-421-6
US-10-364-081-11
US-10-364-081-11
US-10-364-081-11
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Pred. No. 2.2e-143;
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Result No.

Score

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Minimum Maximum

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Total number

Scoring table:

Perfect score:

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RESULT 3

US-10-394-322A-52

Sequence 52, Application US/10394322A

Publication No. US20030232391A1

GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
APPLICANT: Prescott, John C.

TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US

CURRENT APPLICATION NUMBER: US/10/394,322A

CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: US 60/366,892

PRIOR APPLICATION NUMBER: US 60/366,892
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CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 313
TYPE: PAT
ORGANISM: Homo sapiens
US-10-081-119-18
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APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
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No. US20030045491A1
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Pred. No. 2.2e-143;
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US-10-348-081-13
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KORN, MARCUS
APPLICANT: MUBLIER, Guenter
APPLICANT: SCHANK, Georg
APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT PILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOPTWARE: PATENTIN Version 3.2
SEQ ID NO 13
LENGTH: 313
TYPE: PRT
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Best Local Similarity
Matches 313; Conserv
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                                     ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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             ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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240 240 180 120

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; ORGANISM: Homo sapiens US-10-394-322A-52
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PFEHDEETIRGOVFFRORVSSECOHLIRWCLALRPSDRPTFEETONHPWMODVLLPOETA
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo s
US-10-664-421-1
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APPLICANT: MILBURN, MICHAEL V.
APPLICANT: MILBURN, MICHAEL V.
FITTLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-20
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
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US-10-664-421-1
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 Sequence 150, Application US/10664421
Publication No. US20040142864A1
GENERAL INFORMATION:
APPLICANT: BREMER, RYAN
APPLICANT: KUMAR, ABHINAV
APPLICANT: KUMAR, ABHINAV
APPLICANT: KUMAR, ABHINAV
APPLICANT: MANDIYAN, VALSAN
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APPLICANT: BRAHIM, PRAE
APPLICANT: KUMAR, ABHINA
APPLICANT: MANDIYAN, VAL
APPLICANT: MILBURN, MICH
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Best Local Similarity 100.0%;
Matches 313; Conservative C
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Pred. No. 2.2e-143;
0; Mismatches 0; Indels 0
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; TYPE: PRT
; ORGANISM: Homo s
US-10-705-757-2
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SEQ ID NO 150
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
                                              Query Match
Best Local Similarity
                                Matches
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APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PII
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
RUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10705757
Publication No. US20040146942A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                        APPLICANT: GRUENENTHAL GMBH
TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE (
FILE REFERICE: 0.02910.52818US
CURRENT APPLICATION NUMBER: US/10/705,757
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/EP02/05234
PRIOR FILING DATE: 2002-05-13
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: DE 101 23 055.9
PRIOR PILING DATE: 2001-05-11
NUMBER: OF SEQ ID NOS: 11
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100.0%; Score 1670; DB 4; llarity 100.0%; Pred. No. 2.2e-143; Conservative 0; Mismatches 0;
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US-10-377-268-9
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PRIOR FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: 60/360,651
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN Ver: 2.1
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Best Local S
Matches 313
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CURRENT APPLICATION NUMBER: US/10/377,268
CURRENT FILING DATE: 2003-02-28
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                                                       ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                               ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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100.0%; Pred. No. 2.2e-143;
tive 0; Mismatches 0;
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           Sequence 18, Application US/10951406
Publication No. US20050059630A1
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
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US-10-951-406-18
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US-10-951-389-18
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APPLICANT: Reinhard, Christoph
APPLICANT: Vefferson, Anne B.
APPLICANT: Usefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
CURRENT APPLICATION NUMBER: US/10/951,389
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
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Best Local Similarity 100.0%;
Matches 313; Conservative 0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
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                          EIHLHSLSPGPSK 313
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Pred. No. 2.2e-143;
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RESULT 11

US-10-951-477-18

Sequence 18, Application US/10951477

Publication No. US20050063974A1

GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic TITLE OF INVENTION: Target in Cancer FILE REFERENCE: 16932.002

CURRENT APPLICATION NUMBER: US/10/951,477

CURRENT FILING DATE: 2004-09-27

PRIOR APPLICATION NUMBER: US/10/081,119

PRIOR APPLICATION NUMBER: US/10/081,119

PRIOR APPLICATION NUMBER: US/10/081,119

PRIOR APPLICATION NUMBER: US/10/081,119

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US/10/081,119

PRIOR APPLICATION NUMBER: US/10/081,119

PRIOR FILING DATE: 2001-02-21

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 313
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PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR PILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
TYPE: PRT
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US-10-951-406-18
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                                                                 Conservative
                                                             100.0%; Score 1670; DB 5;
100.0%; Pred. No. 2.2e-143;
tive 0; Mismatches 0;
                                                                                               Length 313;
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo s
US-10-977-087-18
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APPLICANT: Khoja, Hamiduddin
APPLICANT: Shyamala, Venkatakrishna
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTI
TITLE OF INVENTION: AND THEIR METHODS OF US
FILE REFERENCE: 2300-21986
CURRENT APPLICATION NUMBER: US/10/977,087
CURRENT FILING DATE: 2004-0-28
PRIOR APPLICATION NUMBER: 10/081,119
PRIOR APPLICATION NUMBER: 60/271,254
PRIOR APPLICATION NUMBER: 60/271,254
PRIOR APPLICATION NUMBER: 10/360,848
PRIOR APPLICATION NUMBER: 10/360,848
PRIOR APPLICATION NUMBER: 10/360,848
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APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
                                                                                                                                                                         SOFTWARE: FastSEQ
SEQ ID NO 18
Query Match 100.0%; Score 1670; DB 5; Best Local Similarity 100.0%; Pred. No. 2.2e-143; Matches 313; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/10977087
Publication No. US20050130926A1
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PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2003-02-06
PRIOR APPLICATION NUMBER: 09/570,593
PRIOR FILING DATE: 2000-05-12
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                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2003-10-30
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                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/626,301
FILING DATE: 2000-07-25
APPLICATION NUMBER: 60/148,936
FILING DATE: 1999-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 10/763,692 FILING DATE: 2004-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/134,112 FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/145,612
                                                                                                                                                                                                                                                                                 FILING DATE: 1999-07-26
APPLICATION NUMBER: 10/698,959
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                                        Length 313;
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Gaps

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APPLICANT: ARTIS, DEAN R.
APPLICANT: BREWER, RVAN E.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: HURT, CLARENCE R.
APPLICANT: HURT, CLARENCE R.
APPLICANT: ZUCKERMAN, REBECCA L.
APPLICANT: ZUCKERMAN, REBECCA L.
TITLE OF INVENTION: WOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT FILE REFERENCE: 039363-1702
CURRENT FILING DATE: 2004-09-15
CURRENT APPLICATION NUMBER: US/10/941,635
CURRENT FILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PATENTING LOTE: 3.2
SEQ ID NO 1
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-941-635-1
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US-10-941-635-1
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Best Local S
Matches 313
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                                                                                                                                                                                                                                                                                                                              Local Similarity
                  241
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100.0%; Pred. No. 2.2e-143;
tive 0; Mismatches 0;
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 Sequence 22, Application US/10620052A
Publication No. US20040126784A1
GENERAL INFORMATION:
APPLICANT: Hitoshi, Yasumichi
APPLICANT: Jenkins, Yonchu
APPLICANT: Markovtsov, Vadim
APPLICANT: Rigel Pharmaceuticals, Ir
```

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GENERAL INFORMATION:

APPLICANT: ARTIS, DEAN R.

APPLICANT: GILLETTE, SAMUEL J.

APPLICANT: GILLETTE, SAMUEL J.

APPLICANT: HURT, CLARENGE R.

APPLICANT: ZUCKERMAN, REBECCA L.

APPLICANT: ZUCKERMAN, REBECCA L.

TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVE FILE REFERENCE: 039363-1702

FULL REFERENCE: 039363-1702

FUL
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US-10-941-635-152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 313; Conservative (
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EIHLHSLSPGPSK 313
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Pred. No. 2.2e-143;
); Mismatches 0;
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Jenkins, Yonchu Markovtsov, Vadim Rigel Pharmaceuticals,

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; TITLE OF INVENTION: Modulators of Cellular Proliferation
; FILE REFERENCE: 021044-004010US
; CURRENT APPLICATION NUMBER: US/10/620,052A
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/395,443
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 313
; TYPE: PRT
; ORCANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PIM1 oncogene serine threonine kinase
US-10-620-052A-22
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Search completed: May 4, 2006, 05:32:05 Job time: 94.6667 secs
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Matches 311; Conserv
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                                                                                 EIHLHSLSPGPSK 313
                                                                                                                                               PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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                                                                EIHLHSLSPGPSK 313
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November 2005

available for processing searches. reduce the amount of time required for their daily updates. This results in more machine time being Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to

applications make up the Published Applications Main databases. Newly published applications will appear in the Published_Applications_New databases; older published

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New). .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New). Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /SIDS5/ptodata/2/pubpaa/USO8 NEW_PUB.pep:*

2: /SIDS5/ptodata/2/pubpaa/USO6 NEW_PUB.pep:*

3: /SIDS5/ptodata/2/pubpaa/USO7 NEW_PUB.pep:*

4: /SIDS5/ptodata/2/pubpaa/USO8 NEW_PUB.pep:*

5: /SIDS5/ptodata/2/pubpaa/USO8 NEW_PUB.pep:*

6: /SIDS5/ptodata/2/pubpaa/USO9 NEW_PUB.pep:*

7: /SIDS5/ptodata/2/pubpaa/USO9 NEW_PUB.pep:*

8: /SIDS5/ptodata/2/pubpaa/USO9 NEW_PUB.pep:*

9: /SIDS5/ptodata/2/pubpaa/USO1 NEW_PUB.pep:*

9: /SIDS5/ptodata/2/pubpaa/USO1 NEW_PUB.pep:*

10: /SIDS5/ptodata/2/pubpaa/USO1 NEW_PUB.pep:*

11: /SIDS5/ptodata/2/pubpaa/USO1 NEW_PUB.pep:*

12: /SIDS5/ptodata/2/pubpaa/USO9 NEW_PUB.pep:*
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length: 2000000000
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1670
    235405 seqs, 46284737 residues
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Copyright (c) 1993 - 2006
    BB
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                         3 US-10-511-937-2982

US-10-501-841-32

US-10-877-346-74

US-10-505-928-690

US-10-501-035-357

US-11-241-056-11

US-11-087-099-9116

US-11-087-099-11500

US-11-087-099-397

US-11-087-099-3612

US-11-087-099-3612

US-11-087-099-3612

US-11-087-099-3612

US-11-087-099-3612

US-11-087-099-3612

US-11-087-099-3612

US-11-087-099-3612

US-10-784-004-951

US-10-784-004-951
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US-10-501-841-40
US-11-103-065-2
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Biocceleration Ltd
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Sequence 435, App
Sequence 951, App
Sequence 11838, A
Sequence 37, Appl
Sequence 67, Appl
                                                               Sequence 2, Appli
Sequence 2982, Ap
Sequence 32, Appl
Sequence 74, Appl
Sequence 550, App
Sequence 11, Appl
Sequence 11, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 183, App
Sequence 1997, Ap
Sequence 3997, Ap
Sequence 3612, Ap
Sequence 312, Ap
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Sequence 40, Appl
Sequence 2, Appli
Sequence 2982, Ap
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325.5	325.5	325.5	326.5	327	327	328	328.5	332	332	333.5	336.5	36	337.5	339	339	339	339	339	339.5	340	341	342	342.5
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US-10-055-877-149	US-10-370-959-31	US-10-370-959-17	US-11-087-099-905	US-11-096-568A-32895	US-10-979-095-6	US-11-151-601-4	US-10-204-639-65	US-11-096-568A-20430	US-11-096-568A-20431	US-11-087-099-1886	US-11-096-568A-18364	US-11-096-568A-32575	US-10-204-639-17	US-10-995-561-877	US-10-995-561-876	US-10-995-561-880	US-10-995-561-878	US-10-995-561-881	US-11-087-099-12331	US-11-087-099-3898	US-11-087-099-11726	US-11-096-568A-22124	US-11-177-138-10
149	31,	Sequence 17, Appl	Sequence 905, App	Sequence 32895, A	Sequence 6, Appli	Sequence 4, Appli	65,			1886,	Sequence 18364, A	ው				Sequence 880, App	Sequence 878, App	Sequence 881, App	12331,	Sequence 3898, Ap		Η	Sequence 10, Appl

ALIGNMENTS

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Sequence 373, Application US/10784004

Publication No. US20060084066A1

GENERAL INFORMATION:

APPLICANT: Biogen Idec

TITLE OF INVENTION: Surrogate Markers of Pain

FILE REFERENCE: 08201.6029-00000

CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT FILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 1251

SOFTWARE: Patentin version 3.2

SEQ ID NO 373

LENGTH: 455

TYPE: PRT

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US-10-784-004-373
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Best Local Similarity
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368
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                                                                                                                                                                                                                                                                             1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
               VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
                                                            FLLVLERPEPAQDLEDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV
                                                                                                                                            FVLILERPEPVQDLFDFITERGALQEBLARSFFWQVLEAVRHCHNCGVLHRDIKDENILI
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 VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM
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RESULT

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Sequence 2, Application US/11103065
Publication No. US20050282189A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel E., Lora, Jose M.
TITLE OF INVENTION: 2150, Human Protein Kinase Family
TITLE OF INVENTION: Member and Uses Therefor
FILE REFERENCE: MPI2001-137PIRNM
CURRENT APPLICATION NUMBER: US/11/103,065
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR FILING DATE: 2001-06-28
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 10/057,475
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
LENGTH: 311
TYPE: PRT
ORGANISM: Homo sapiens
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Best wecal Similarity
Matches 167; Conserv
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APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Coriosation
TITLE OF INVENTION: Compositions and Methods for the Detection,
TITLE OF INVENTION: and Therapy of Hematological Malignancies
FILE REFERENCE: 014058-014402PC
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Clapper, Jonathan David
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ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
ITILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CCURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOPTWARE: PatentIn version 3.2
SEQ ID NO 2982
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Best Local Similarity
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                           163;
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28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP
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Prentice, James
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                                                                                                                                                                                                      51.7%; Score 864; DB 8; illarity 61.3%; Pred. No. 5.5e-66; Conservative 37; Mismatches 64
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RESULT 6
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US-10-501-841-32
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Best Local S
Matches 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis TITLE OF INVENTION: and Therapy of Hematological Malignancies FILE REFERENCE: 0.14058-014402PC
CURRENT APPLICATION NUMBER: US/10/501,841
CURRENT FILING DATE: 2004-07-14
PRIOB APPLICATION NUMBER: US 10/057,475
PRIOR APPLICATION NUMBER: US 10/057,475
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
PRIOR FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 124
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ORGANISM: Homo sapiens
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                                                                                                                                           VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261
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Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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PRIOR APPLICATION NUMBER: 00/235,633
PRIOR APPLICATION NUMBER: 05/235,631
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 98; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 127
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CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
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APPLICANT: Spyrek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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APPLICATION NUMBER: 60/237,434
FILING DATE: 2000-10-03
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APPLICATION NUMBER: 60/236,066
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APPLICATION NUMBER: 60/236,065
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APPLICATION NUMBER: 60/236,064
172
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                       RYHRYHGRSAAVWSLGILLYDMVCGDIPF---EHDEEIIRGQVFFRQRV------SSECQ
                                                                                                    HCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVY---TDFDGTRVYSPPEWI
EGRGYSSK-VDVWSLGVILYELLTGKLPFPGIDPLEELFRIKERPRLRLPLPPNCSEELK
                                                                               YLHSRGIVHRDLKPENILLDEN-GTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL
                                                                                                                                                            --HPNIVRLLGVFEEDDHLYLVMEYMEG-GDLFDYLRRNGLLLSEKEAKKIALQILRGLE 112
                                                                                                                                                                                                SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERG-ALQEELARSFFWQVLEAVR
                                                                                                                                                                                                                                             YELGEKLGSGAFGKVYKGKHKDTGEIVAIKILKKRSLSE-----KKKRFLREIQILRRLS
                                                                                                                                                                                                                                                                                 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS
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Smithson, Glennda
Millet, Isabelle
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Stone, David
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Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ellerman, Karen
Grosse, William M
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                                                                                                                                                                                                                                                                                                                            Conservative
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37.0%; Pred. No. 2.56
tive 46; Mismatches
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nes 98;
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US-10-501-035-357; Sequence 357, A; Publication No.
; ORGANISM: Homo sapiens US-10-501-035-357
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-690
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US-10-505-928-690
                                    APPLICANT: Briscol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
TITLE OF INVENTION NUMBER: US/10/501,035
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US 60/350,061
PRIOR APPLICATION NUMBER: US 60/350,061
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOPTWARE: Patentin version 3.2
SEQ ID NO 357
LENGTH: 950
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PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 690
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 VLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFG-SGALLKDTVYTDFDGTRVYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 EIMS--SLNHPHIISIYEVFENKDKIVIIMEYASK-GELYDYISERRRLSERETRHFFRQ
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Pred. No. 1.2e-24;
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Publication No. US20060024807A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Virca, G. Duke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1 SEQ ID NO 11
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Best Local
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Best Local Similarity
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CURRENT FILING DATE: 2005-09-30
PRIOR APPLICATION NUMBER: US/09/980,464
PRIOR FILING DATE: 2001-11-27
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 631
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157
                                    244 HDE-----EIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
                                                                                                                                    185 IDFG-SGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFE 243
                                                                                                                                                                                 138 R-GDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDAN-GNIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 LALRPSDRPTFEEIQNHPWM-----QDVLLPQE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 -- HPHIKLYOVMETKSMLYLVTEYAKN-GEIFDYLANHGRLNESEARRKFWQILSAVDY 156
                                                                                                                                                                                                                          125 PVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 LVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 RYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIIRGQVFFRQRVSSECQHLIRWC 270
                                                                                                                                                                                                                                                                          83 AIKSIRKDKIKDEQDL---LHIRREIEIMS--SLNHPHIIAIHEVFENSSKIVIVMEYAS
                                                                                                                                                                                                                                                                                                                      65 AIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPE 124
                                                                                                                                                                                                                                                                                                                                                                   24 ARPLADGLIKSPKPLMKKQAVKRHHKHNLRHRYEFLETLGKGTYGKVKKA-RESSGRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
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GQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATLEDVASHWWV
                                                                                        ADFGLSNLYHKGKFLOTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILVHGTMPFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL----DAVNLEKIYREVQIMKMLD 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEGQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Martin, Unja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 368.5; DB 11;
Pred. No. 1.7e-23;
6; Mismatches 116;
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; Sequence 9816, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION UMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-10-877-346-72
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APPLICANT:
APPLICANT:
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LENGTH: 504
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                         APPLICANT:
                   PRIOR
                                               CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/964,956
PRIOR FILING DATE: 2001-09-26
                                                                                                                    APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic
FILE REFERENCE: 21402-124
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                APPLICATION NUMBER: 60/235,631 FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/235,633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 YQVGPLLGSGGFGSVYSGIRVSDNLFVAIKHVEKDRISDWGELFNGTRVFMEVVLLKKVS
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                                                                                                                                                                                                                                                                                                                                                                                                  Gerlach, Valerie L
MacDougall, John R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----IRGQVF-FRQRVSSECQHLIRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLALRPSDRPTFEEIQNHPWMQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH
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Smithson, Glennda
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK
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                                                                                                                                                                                                                        Lepley, Denise M
Burgess, Catherine E
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                     Ellerman, Karen
Grosse, William M
Alsobrook II, John P
                                                                                                                                                                                       Kekuda, Ramesh
Spytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                                 Millet, Isab
Stone, David
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                                                                                                                                                                        Leach, Martin D
                                                                                                                                                                                                                                                                                                                             Gunther, Erik
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Pred. No. 2.1e-23;
1; Mismatches 105;
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                                                                                                                                    Encoding
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CURRENT APPLICATION NUMBER: US/11/113,42
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR RILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR FILING DATE: 2001-08-29
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                                                                                                                                                                                                                                                                                                  Sequence 183, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                    APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic
FILE REFERENCE: 21402-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-05
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Serine/Threoniune protein kinase Co
OTHER INFORMATION: Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                          229 AKDLIKKLIVKDPEKRLTAEEALEHPF
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Pred. No. 1.2e
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)8 EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 11500
LENGTH: 514
TYPE: PRT
ORGANISM: Lycopersicon esculentum
US-11-087-099-11500
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US-11-087-099-11500
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PRIOR FILING DATE: 2001-07-24
PRIOR PPLICATION NUMBER: 60/322,358
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR APPLICATION NUMBER: 60/288,153
PRIOR APPLICATION NUMBER: 60/288,153
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11500, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 190
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 183
LENGTH: 256
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Best Local
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Best Local Similarity
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                   Similarity
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                                   SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH
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Pred. No. 1.2e-23;
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Pred. No. 1.6e-22;
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Sequence 3997, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3997
LENGTH: 512
TYPE: PRT
ORGANIAM: Solanum tuberosum
                                                  APPLICANT: Abad, Mark S. et al.
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) SUS 1P
CURRENT APPLICATION UNMERR: US 1P
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3612
LENGTH: 514
TYPE: PRT
ORGANISM: Solanum tuberosum
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Publication No. US20060041961A1
GENERAL INFORMATION:
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Query Match
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21.1%;
Score 352;
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Search completed: May 4, 2006, 05:32:56 Job time: 16.3333 secs
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                                                252 LIVDPMKRMTIPEIRLHPWFQ 272
                                   271 LALRPSDRPTFEEIQNHPWMQ 291
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Maximum DB
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2: geneseqp1990s:*
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5: geneseqp2002s:*
6: geneseqp2003ss:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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ALIGNMENTS

ated to tyrosine threonine kinase (TTK, see ABP54938). TTK ynucleotides and polypeptides of the invention encompass ynucleotides and polypeptides having sequence similarity or nitty to human TTK and other genes and gene products relate has Piml. The invention is based on the finding that TTK i ferentially expressed in various forms of cancer. It provid the identification of cancerous cells, especially breast of the identification of cancerous cells, especially breast or cancer cells, by detection of expression levels of TTK.	PT abnormal expression levels and activity of TTK, such as lung, col PT prostate and ovarian cancer. XX PS Disclosure; Page 80-81; 113pp; English. XX CC The present semience is the protein semience of human Diml. a pro-	WPI; 2002-698650/75. N-PSDB; ABV73989. Reducing growth of cancer cells comprises reducing the control of the	21-FEB-2001; 2001US-0271254P (CHIR) CHIRON CORP.	Homo sapiens. W0200268444-A 06-SEP-2002.	XX DE Human Piml. XX XX XX KW Piml; tyrosine threonine kinase; TTK; protein kinase; enzyme; KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostat KW human; gene therapy.	ABP54943 ID ABP54943 standard; protein; 313 AA. XX AC ABP54943; XX DT 13-JAN-2003 (first entry)

The present sequence is the protein sequence of human Piml, a protein related to tyrosine threonine kinase (TTK, see ABP54938). TTK polynucleotides and polypeptides of the invention encompass polynucleotides and polypeptides having sequence similarity or sequence identity to human TTK and other genes and gene products related to TTK, such as Piml. The invention is based on the finding that TTK is differentially expressed in various forms of cancer. It provides methods for the identification of cancerous cells, especially breast cancer and colon cancer cells, by detection of expression levels of TTK, as well as

Reducing growth of cancer cells comprises reducing Tyrosine Threonine Kinase (TTK) activity, useful in diagnosing and treating disorders with abnormal expression levels and activity of TTK, such as lung, colon, prostate and ovarian cancer.

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                            Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
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23-AUG-2000; 2000US-00644450.
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                                                                                               CHEF ) GRUENENTHAL GMBH
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(REIN/)
(JEFF/)
(CHAN/)
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  ) REINHARD C.
) JEFFERSON A
) CHAN V W.
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Reinhard C,
2003-456566/43
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N-PSDB; ACA62265

normal is indi ing cancer in a subject, by comparing expression levels of tyrosine ine kinase polypeptide or polynucleotide in a subject cell and a cell, where an increase in the expression level in the test cell

Disclosure; Page 34-35; 79pp; English.

CC threonine kinase (TTK, a mirotic checkpoint gene) polypeptide or polynucleotide in a test cell obtained from the subject and in a normal connectate cell, where an increase in the expression levels of tyrosine connectates the presence of cancer other than ovarian cancer and in a normal connectates the presence of cancer other than ovarian cancer. Also included are reducing growth of a cancerous cell (by contacting a cancerous cell contacting a cancerous cell (contacting a cancerous cell (provided activity of a growth of a cancerous cell (comprising: (i) detecting the activity of TTK polypeptide in the presence of a candidate agent that reduces capent), identifying an agent that reduces TTK activity of a contacting a cancerous cell (comprising: (i) detecting the activity of TTK polypeptide activity in the absence of a candidate agent capent; in its polypeptide activity in the absence of the candidate agent (contacting a cancerous cell displaying elevated expression of a TTK contacting a cancerous cell displaying elevated expression of a TTK contacting a cancerous disease other than ovarian cancer in a contacting a cancerous disease other than ovarian cancer in a contactivity of expression of TTK -encoding polynucleotide in a test cancer cell where the level of expression of TTK in the test cancer cell with prognosis of the polynucleotide in the cancerous disease). The methods are cell creduces growth of a cancerous cells, identifying an agent that cancer cell creduces growth of a cancerous cells, identifying a candidate agent that control non-cancer cell is condicative of the prognosis of the polynucleotide in the test cancer cell creduces growth of a cancerous cells, identifying an agent that reduces TTK condicative of the prognosis of the cancerous disease). The methods are creduced to the cancer cell is condicated the reduces TTK condicated to respond to a particular therapy expension of the cancerous disease other than cancer cell creduced to the cancer cell is condicated to the cancer cell is condicated t The invention relates to detecting cancer (other than ovarian can a subject, comprising comparing the expression levels of tyrosine cancer) ij

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Query Match Best Local Similarity

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Matches 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agent for treating
                                                                                                                                                                                                                                                                                           The present sequence is the protein sequence of the human serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the paralogues of novel human and murine PIM-3 proteins (see ABR62932 and ABR62933) of the invention, which are therefore expected to be involved in cancer and cell growth regulation. PIM-3 is also involved in the development of insulin resistance and type 2 diabetes mellitus. The invention relates to the use of PIM-3 nucleic acids and proteins in: screening assays for compounds that modulate insulin resistance or type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing, forensic biology); predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, pharmacogenomics); and for the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. diagnostic or prognostic assays, monitoring clinical trials, pharmacogenomics); and for the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus (e.g. diagnostic or prognostic assays).
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                                                                                                                                                                                                                                                     Sequence 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human or murine PIM-3 DNAs or polypeptides, useful for nt for identifying anti-type 2 diabetes mellitus drugs, ating insulin resistance or type 2 diabetes mellitus.
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                                                           NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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           C claimed are a vector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC wit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal cC that is differentially expressed in neuronal tissue of a first animal cC the expression of a polynucleotide sequence which regulates to the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a cC method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of the compound that regulates its activity is useful for preparing a medicament for treating condulates its activity is useful for preparing a medicament for treating condulates its activity is useful for preparing a medicament for treating condulates its activity is useful for preparing a medicament for treating condulates its activity is useful for preparing a medicament for treating condulates.
                                                                                                                                                                                                                                                                                                                                     The invention discloses a composition comprising two or more is or human polynucleotides or a polynucleotide which represents a derivative or allelic variation of the nucleic acid sequence. A
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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BAYER AG.
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Matches 313
                                                                  Identifying ligand binding to inact kinase (T) comprises contacting the contains reactive group at binding kinase-ligand conjugate formation.
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therapy).
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                                                                                                                                                                                                                                                Prescott
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Pred. No. 1.4
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ng the conformation modified (T) which 
nding site, with ligands and detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibitor; PIM1
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L.4e-154;
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Best Local S
Matches 313
                                                                                                                                                                                                                                         Human; PRO; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; systemic acclerosis; Sjogren's autoimmune thrombocyropenia; thyroiautoimmune haemolytic anaemia; autoimmune thrombocyropenia; thyroiautoises mellitus; renal disease; demyelinating disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method for identifying a ligand (L) which binds to an inactive conformation of target protein kinase (T). method involves contacting inactive conformation of (T), which contain or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bending to the reactive group thus forming a kinase-(L) conjugate (C) The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
                                           08-NOV-2002;
                                                                                                                                     WO2004043361-A2
                                                                                                                                                                    Homo
                                                                                                                                                                                                   chronic inflammatory
                                                                                                                                                                                                              demyelinating
                                                                                                                                                                                                                                central nervous
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ilarity 100.0%;
Conservative 0
                                             2002US-0425235P
                                                                        2003WO-US035268
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                                                                                                                                                                                            us system; peripheral nervous system; polyneuropathy; Guillain-Barre syndrome; mmatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
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Pred. No. 1.4e-154;
Mismatches 0;
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Best Local S
Matches 313
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                                                           Molecular
G-protein
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                               Homo sapiens
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Wu TD;
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                                                           scaffold; nuclear hormone receptor; TNF receptor coupled receptor; methyl transferase; ligase; PII
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Best Local Similarity
Matches 313; Conserv
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20-SEP-2002;
02-JAN-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 313 AA;
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                                                                                     PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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 EIHLHSLSPGPSK 313
                               EIHLHSLSPGPSK 313
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                                                              PFEHDEETIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEETQNHPWMQDVLLPQETA
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; 2002US-0412341P.
; 2003US-0437929P.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory, antiarthritic, autiliumus, someteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, osteopathic, antidiabetic, antidiabetide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediatrenal disease, or demyelinating diseases of the central or peripheral
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N-PSDB; ADP24226.
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llarity 100.0%;
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Pred. No. 1.4e-154;
Mismatches 0;
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Best Local Similarity
                                                                                                                                 The invention relates to a method of screening a prophylactic-therapeutic agent for an apoptosis inducing agent or an enhancer of an anticancer agent. The method involves the use of a serine/threonine kinase pim-1, its partial peptide or its salt. Also disclosed is a kit for carrying out the method of the invention. The method is useful for screening a prophylaxis and/or treatment of cancer. The method is also useful for prophylaxis and/or treatment of cancer, inducing apoptosis, treating a patient having a solid tumour that is resistant to an anticancer agent
                                            Sequence 313
                                                                                      (induced by hypoxia), and for screening a substance that promotes or inhibits the activity of serine/threonine kinase Pim-1. The present sequence represents a human polypeptide relating to the present
                                                                                                                                                                                                                                                                                                        Screening for a prophylactic-therapeutic apoptosis inducing agent or enhancer of anticancer agent, comprises use of serine/threonine kinase Pim-1, its partial peptide or its salt.
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DB; ADT07366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ONCOREX INC
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                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                   Jian C;
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100.0%;
Score 1670; DB 8;
Pred. No. 1.4e-154;
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Pim-1; cancer;
              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     solid tumour
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RESULT 12
ADT14636
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                                                    04-APR-2003; 2003US-0460843P
12-MAR-2004; 2004US-0552526P
                                                                               01-APR-2004; 2004WO-US010345
                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                    crystallography; Pim-1; cancer; serine/threonine kinase;
protein co-ordinate data; protein structure.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADT14636 standard; protein; 313
WPI; 2004-757977/74
                Jacobs ML,
                                                                                                                   WO2004090106-A2
                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                      Domain
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                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                               human Pim-1
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                                  (VERT-) VERTEX
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                Hare B,
                                                                                                                                                                                                                                                                                                                                                              (oncogene-encoded serine/threonine kinase) protein.
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                   PHARM INC.
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                 /label= OTHER
/note= "OTHER = Forms a salt bridge via linkage to
Arg166"
                                                                                                                                                                      note = Activation
                                                                                                                                                                                                 /label= OTHER
/note= "OTHER
                                                                                                                                                                                                                                                             note = Glycine-rich
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                Swenson L;
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Crystal useful for developing Pim-1 (oncogene-encoded serine/threonine kinase) inhibitors, comprises human Pim-1 protein, Pim-1 homologue, human Pim-1 protein complex, or Pim-1 homologue complex.
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SEQ ID NO 2; 219pp; English.

The invention relates to a novel crystal comprising a human Pim-1 (Oncogene-encoded serine/threonine kinase) protein, a Pim-1 homologue, human Pim-1 protein complex or a Pim-1 homologue complex. Pim-1 is primarily expressed in haemopoietic and germ cell lines and this expression is tightly regulated and induced by cytokines, mitogens and hormones. Human Pim-1 is associated with multiple cellular functions, such as proliferation, differentiation, apoptosis and tumourigenesis. To crystal of the invention relates particularly to the residues involved the active site and binding sites of Pim-1. Such information may be useful for developing Pim-1 inhibitors that are useful as therapeutic agents in the treatment of cancer. The current sequence is that of the human Pim-1 (oncogene-encoded serine/threonine kinase) protein of the The d in ø

Sequence 313 AA;

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Best Local Similarity
Matches 313; Conserv
301
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                                                 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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                                                                                                                                                                                                                             NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
             EIHLHSLSPGPSK 313
                                                                                                                     ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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EIHLHSLSPGPSK 313
                                                                                                       ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                  100.0%; Score 1670; DB 8; 100.0%; Pred. No. 1.4e-154; vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           Length
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RESULT 13
ADY86782
ID ADY86
XX ADY86
XX ADY86
XX ADY86
XX P102-JU
XX Progr
KW Progr
KW Pinl.
XX Pinl.
XX US20(
XX US20(
XX XX
PF 27-SI
XX

Prognosis; Human 02-JUN-2005 ADY86782;

cancer; protein,

cytostatic; neoplasm; tyrosine threonine kinase;

TTK;

Pim1

SEQ ID NO:

18

(first entry)

Homo sapiens

27-SEP-2004; 2004US-00951477

24-MAR-2005.

ADY86782 standard; protein; 313 AA

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RESULT 14
AEA89424
ID AEA89
XX
AC AEA89
AC AEA89
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DT 25-AU
XX
DT 25-AU
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DE Humar
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KW Drug
KW Pim11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2001;
23-FEB-2001;
21-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assessment of prognosis of a cancerous disease other than ovarian comprises detection and comparison of expression of a tyrosine thr kinase-encoding polynucleotide in a test cancer cell with a contro cancer cell.
                                      Human Pim1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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             screening;
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JEFFERSON
CHAN V W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                             standard; protein;
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                                                                                                                                                                                             EIHLHSLSPGPSK
                                                                                                                                                                                                                              PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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                                    protein,
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(llarity 100.0%;
Conservative (
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2001US-0289813P.
2002US-00081119.
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             diagnosis;
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                                     SEQ ID NO:
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            therapeutic;
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Pred. No. 1.4e-154;
Mismatches 0;
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             cancer;
            cytostatic;
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21-FEB-2002;
06-FEB-2003;
30-OCT-2003;
                                                                                                                                                                                                                                                                                                                 The invention relates to human HX2004-6 protein and a seven transmembrane receptor protein referred as VSHK-1 useful for diagnosing or treating cancer. The invention also relates to a method for reducing the growth of a cancerous cell. VSHK-1 is useful for identifying a VSHK-1 receptor ligand and to identify a substance which modulates its signal transduction activity. The HX2004-6 DNA is useful to detect the presence of HX2004-6 in a biological sample (e.g. ductal epithelial cells from tissue chosen from pancreas, colon and breast). The invention is useful for screening drugs for the treatment of cancer. The present sequence is the human piml protein. This sequence is differentially expressed in
                                                                                                                                                                                                                                                                                  Sequence 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 18; 206pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human HX2004-6 polypeptide o useful for diagnosing or treating cancer, identify a VSHK-1 receptor ligand.
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03-NOV-1999;
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26-JUL-1999;
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06-JAN-1999;
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25-JUL-2000;
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                                                                                                ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                    ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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2003US-00360848.
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1.4e-154;
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Best Local Similarity
Matches 313; Conserv
                                                                                                                                                                                                                                                                                         The invention relates to a novel method for identifying substances that regulate urinary incontinence and the urge to urinate. The method comprises incubating a test compound with a cell and/or cell preparation that has synthesized a specific protein of the PIM (proviral integration site) kinase family and measuring either binding of the test compound to the PIM kinase, or a functional parameter that is altered by the binding. The method of the invention demonstrates uropathic and gene therapy applications and may be useful for treatment and diagnosis of urinary incontinence and the urge to urinate. The method is based upon regulating the activity or expression of PIM kinases that are involved in bladder control. The current sequence is that of the human PIM-1 serine-threonine
                                                                                                                                                                                                                                                Sequence 313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying substances that regulate PIM kinases, useful for treatment and diagnosis of urinary incontinence and the urge to urinate, and similar use of PIM proteins or nucleic acids.
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N-PSDB; AEB96036.
REFSEQ; NP_002639.
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                                                                    NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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ALIGNMENTS

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A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon: C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncoge:	A;Gene: GDB:PIM1 A;Gross-references: GDB:119495; OMIM:164960 A;Cross-references: GDB:119495; OMIM:164960 A;Map position: 6p21.2-6p21.2 A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1 C:Function:	A;Status: prelnninary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-313 <doms a;cross-references:="" at="" autophosphorylates="" c:gengetics:<="" c;comment:="" gb:m54915;="" nid:g189961;="" pim-1="" sites.="" td="" uniparc:upi0000001060;="" unknown=""><td>A;Title: Comparison of the human and mouse PIM-1 cDNAs: A;Reference number: I58412; MUID:88217305; PMID:3329709 A;Accession: I58412</td><td>A; PIOLECULE CYPE: MRNA A; Residues: 1-14, 'RA', 17-313 < ZAK> A; Cross-references: UNIPARC: UPIO00014987C; GB: M16750; NID: g189956; PIDN: AAA60089.1; A; Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.</td><td>R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A. Gene 54, 105-111, 1987 A;Title: The CDNA sequence and gene analysis of the human pim oncogene. A;Reference number: A27476; MUID:87277423; PMID:3475233 A;Accession: A27476</td><td>A;Reference number: A46554; MUID:88115604; PMID:3429489 A;Accession: A46554 A;Molecule type: mRNA A;Residues: 1-313 cMES A;Cross-references: UNIDARC:UPI0000001060: GB:M24779: NID:G106:</td><td>A;Cross-references: UNIPROT:P11309; UNIPARC:UPI0000001060; GB:M27903; NID:g189958; R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M. R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.</td><td>Gene 90, 303-307, 1990 A;Title: Primary structure of the putative human oncogene, A;Reference number: JU0327; MUID:90382681; PMID:2205533 A;Accession: JU0327 A;Molecule type:</td><td>: Homo sap 1-Mar-1989 on: JU0327</td><td>ase (</td><td>REGIT T</td><td>ALIGNMENTS</td><td>461 473</td><td>325.5 19.5 442 2 325 19.5 1246 2 324.5 19.4 713 2 324 19.4 401 2</td><td>326.5 19.6 746 2</td></doms>	A;Title: Comparison of the human and mouse PIM-1 cDNAs: A;Reference number: I58412; MUID:88217305; PMID:3329709 A;Accession: I58412	A; PIOLECULE CYPE: MRNA A; Residues: 1-14, 'RA', 17-313 < ZAK> A; Cross-references: UNIPARC: UPIO00014987C; GB: M16750; NID: g189956; PIDN: AAA60089.1; A; Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.	R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A. Gene 54, 105-111, 1987 A;Title: The CDNA sequence and gene analysis of the human pim oncogene. A;Reference number: A27476; MUID:87277423; PMID:3475233 A;Accession: A27476	A;Reference number: A46554; MUID:88115604; PMID:3429489 A;Accession: A46554 A;Molecule type: mRNA A;Residues: 1-313 cMES A;Cross-references: UNIDARC:UPI0000001060: GB:M24779: NID:G106:	A;Cross-references: UNIPROT:P11309; UNIPARC:UPI0000001060; GB:M27903; NID:g189958; R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.	Gene 90, 303-307, 1990 A;Title: Primary structure of the putative human oncogene, A;Reference number: JU0327; MUID:90382681; PMID:2205533 A;Accession: JU0327 A;Molecule type:	: Homo sap 1-Mar-1989 on: JU0327	ase (REGIT T	ALIGNMENTS	461 473	325.5 19.5 442 2 325 19.5 1246 2 324.5 19.4 713 2 324 19.4 401 2	326.5 19.6 746 2
-serine-phosphate or ; protein kinase homo		J 15; NID:g189961; PIDN:AAA36447.1; es.	DNAs: Nucleotide sequence 29709	50; NID:g189956; PI M.; Grosveld, G.;	A. e human pim oncoger 75233	29489	, Š	ncogene, pim-1. 05533	#text_change 09-Ju	† † † † † † † † † † † † † † † † † † †			probable serine/cn serine/threonine-s	nypotnetical prote protein H39E23.1 [probable serine/th SNF1-related prote	probable calcium-d SNF1-related prote

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A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonir A; Note: in testis may be involved in signal transduction events of normal germ cell matu C; Superfamily: kinase-related transforming protein; protein kinase homology C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F; 36-290/Domain: protein kinase homology <KIN> F; 44-52/Region: protein kinase ATP-binding motif F; 67/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Wingett, D.; Reeves, R.; Magnuson, N.S.
Nucleic Acids Res. 20, 3183-3189, 193-
A;Title: Characterization of the testes-specific pim-1 transcript
A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Accession: S26298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming prot
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997
C;Accession: S26298
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A;Note: testis-specific transcript is shorter
C;Comment: Pim-1 autophosphorylates at unknown
C;Function:
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                       ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
                                                           NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
                                                                          NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
                                                                                                                 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
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                                                                                                                                                                         Score 1636; DB 1;
Pred. No. 9.2e-75;
6; Mismatches 3;
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Pred. No. 1.9e-76;
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93.9%;
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A;Cross-references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:g20 C;Comment: Pim-1 autophosphorylates at unknown sites. C;Geneetics:

A;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Function:
C;Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: kinase-related transforming protein; protein kinase homology C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonif;36-290/Domain: protein kinase homology <KINb; F;44-52/Region: protein kinase ATP-binding motif F;67/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The primary structure of the putative oncogene A;Reference number: A24169; MUID:86272109; PMID:3015420 A;Accession: A24169
A;Molecule type: DNA A;Residues: 1-313 <SEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein kinase (BC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1;
C;Species: Mus musculius (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_chang
C;Accession: A24169
R;Selten, G; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.;
Cell 46, 603-611, 1986
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                                 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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Pred. No. 4.4e-72
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C; Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning, protein kinase homology C; Superfamily: kinase-related transforming protein; protein kinase homology C; Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotr. F; 89-345/Domain: protein kinase homology <KIN>F; 89-105/Region: protein kinase ATP-binding motif
                hypothetical protein F45H7.4 - Caenorhabditis elegans C;Speciaes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T22255 # R;Percy, C
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A;Cross-references: UNIPARC:UPI00000278BF; GB:L41495;
A;Note: 34K form
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A; Residues: 'M', 27-370 < VA2>
A; Cross references: UNIPARC: UPI00000278BE;
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A; Start codon: CTG
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A;Molecule type: mRNA
A;Residues: 'M',61-370
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A; Residues: 1-370 < VAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; van der Lugt, N.M.T.; Domen, J.; Verhoeven, EMBO J. 14, 2536-2544, 1995
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Best'Local Sim
Matches 171;
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;Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change 09-Jul-2004
;Accession: S55333; A43093; B43093
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Pred. No. 2.7e-37;
1; Mismatches 85
 June
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                                                  #text_change
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A;Reference number: Z19538
A;Accession: T22255
A;Status: preliminary; translated from A;Molecule type: DNA
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UN
A;Experimental source: clone F45H7
C;Gene: CESP:F45H7.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
A; Introns: 72/3;
C; Superfamily: p
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T15435
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                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, February 1994 A, Description: The sequence of C. elegans cosmid C06E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C06E8.3 - Caenorhabditis C;Species: Caenorhabditis elegans C;Date: 20-Sep_1999 #sequence_revision 20-Sep-C;Accession: T15435
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A;Cross-references: UNI
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                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
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                                                                                                                                                                                              Query Match
Best Local S
Matches 105
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Best Local S
Matches 120
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 115
                              120
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                  LERPEPVQDLFDF1TERGALQEELARSFFWQVLEAVRHCHN-CGVLHRDIKDENILIDLN 178
                                                                                                                                                        MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSG-IRVS
MERPANCMOLFDMVSVHGPLNEDMGKFIFKQVITTVFNMYSKHGLLHRDIKDENLIVNMN
                                                               GQQPVAVKFVQHKHVRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV
                                                                                            DNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLI
                                                                                                                               MIKRKLODLAVCCSYQVDFLHEKK----HSVKEFKRKYEVLDEIGRGGFGIVYEATTROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTFDFFQRCSLEAILNHPWVKQQTL 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHECVQNRVLHRDLKDENIVIDLVTGSTKLIDFGAATVLRRSQYSDFQGTRLYCPPEWFL
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                                                                                                                                                                                                                                                                                                                source:
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76/3;
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ce: strain Bristol N2
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45.3%;
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35.8%;
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                                                                                                                                                                                             Score 486; DB 2
Pred. No. 1.2e-J
5; Mismatches ?
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Pred. No. 3.5e-24;
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                                                                                                                                                                                                                               DB 2;
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RESULT 8
T13741
A;Cross-references: FlyBase:FBgn0000667
A;Introns: 205/3; 227/1; 322/3; 688/3;
A;Note: EG:22E5.8
                                                       A;Residues: 1-1398 <MUR>
A;Cross-references: UNIPROT:077268; UNIPARC:UPI00000820A3; EMBL:AL031765; NID:e1371523; C;Genetics:
                                                                                                                                                                 C;Keywords: ATP
F;71-324/Domain: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed A;Reference number: 149071; MUID:95200798; PMID:7893599
A;Accession: 149072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
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A; Residues: 1-1398 <
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A;Molecule type: mRNA
A;Residues: 1-481 <RES>
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Best Local Similarity
Matches 99; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQ 291
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                   782/3; 814/2; 1363/3
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RESULT 9
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A;Map position: 15L
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A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT:Q08217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwartted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 12-Jul-1996 #sequence_revision C;Accession: S66730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: ATP
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                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
1074
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SLIKRILTREVDKRPTIDEIYEDKWLK 1100
                                  HLIRWCLALRPSDRPTFEEIQNHPWMQ 291
                                                                         FFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRV 206
                                                                                                                                                                                                                                  ATLNKNSQENILKLLDFFEDDDYYYI----ETPVHGETGSIDLFDVIEFKKDMVEHEAKL
                                                                                                                                                                                                                                                                       KKVS-SGFSGVIRLLDWFERPDSFVLILERPEPVQ-----DLFDFITERGALQEELARS 146
                                                                                                                                                                                                                                                                                                              SDFTILOVMGEGAYGKVNLCIHNREHYIVVIKMIFKERILVDTWVRDRKLGTIPSEIQIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLL 295
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                                                                                                            YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFF--RQRVSSECQ 264
                                                                                                                                                     VFKQVVASIKHLHDQGIVHRDIKDENVIVD-SHGFVKLIDFGSAAYIKSGPFDVFVGTMD
                                                                                                                                                                                                                                                                                                                                                   SQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; ne Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            32.6%;
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                                                                                                                                                                                                                                                                                                                                                                                         Score 376; DB 2;
Pred. No. 8e-12;
59; Mismatches 105;
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A;Accession. ...
A;Molecule type: DNA
A;Residues: 1-72,'E',74-154 <SID>
A;Residues: 1-72,'E',74-154 <SID>
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A;Residues: 1-864,867-1358 <OUE>
A;Residues: 1-864,867-1358 <OUE>
A;Cross-references: UNIPARC:UPI0000052EA6; EMBL:L05146; NID:g171851; PIDN:AAC04940.1;
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, Yeast 8, 133-145, 1992
A;Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptic A;Reference number: S22266; MUID:92221690; PMID:1561836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) K;Alternate names: protein YAL002; protein YAL007w; secretory protein SSP138 C;Species: Saccharomyces cerevisiae C;Pate: 30-Sep-1993 #sequence revision 02-Aug-1994 #text_change 05-Oct-2004 C;Accession: S33653; S36717; S36732; JH0486 R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac Yeast 9, 543-549, 1993
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc A;Reference number: S33653; MUID:93311122; PMID:8322517
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F;1104-1112/Region: protein kinase ATP-binding motif
F;8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI000017A44A; EMBL:S93805 R;Sidhu, R.S.; Mathewes, S.; Bollon, A.P. Gene 107, 111-118, 1991 A;Title: Selection of secretory protein-encoding genes by A;Reference number: JH0483; MUID:92077420; PMID:1743509 A;Accession: JH0486
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A;Cross-references: UNIPROT: P31374; UNIPARC: UPI000017A449; EMBL: L05146
R;Ouellette, F; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng,
submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae
A;Reference number: S36711
A;Accession: S36717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SGF
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LRPSDRPTFEEIQNHPWM
                                                                                  GNPYEGOPODIWAIGILLYTVVFKENPFYNIDEILEGDLKFNNAEEVSEDCIELIKSILN
                                                                                                                                                                                                                                     VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIR 214
                                                                                                                                                                                                                                                                                                                                                              SGVIRLLDWFERPDSFVLILERPEPVQ-----DLFDFITERGALQEELARSFFWQVLEA 154
                                                                                                                                                                                                                                                                                                                                                                                                                   MGEGAYGKVNLCIHKKNRYIVVIKMIFKERILVDTWVRDRKLGTIPSEIQIMATLNKKPH
                                                                                                                                                                                            IKHLHDQGIVHRDIKDENVIVD-SKGFVKIIDFGSAAYVKSGPFDVFVGTIDYAAPEVLG
                                                                                                                  YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFR--QRVSSECQHLIRWCLA
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33.7%; Pred.
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R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; submitted to the EMBL Data Library, October 1992 A;Description: Eg3, selected by differential screening
                                                                                                                                                                                                                                                                                                                                      RESULT 12

$52244

$65823 Protein - African clawed frog

$65826 Services: Xenopus laevis (African claw

$C;Date: 07-May-1995 #sequence_revision

$C;Accession: $52244

$C;Accession: $52244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI00000A4B92; EMBL:Y10036
A;Experimental source: cv. Masterpiece; cotyledon
C;Function:
C;Function: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>
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                                                                                                                             A;Cross-references: UNIPROT:Q91821; UNIPARC:UPI000017A463; EMBL:Z17205; NID:g609283; C;Keywords: ATP
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                                                                                  F;19-27/Region:
                                                                                                                                                                       A;Residues: 1-651 <ROG>
                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                           A; Status: preliminary
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Matches 90
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protein kinase ATP-binding
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(African clawed frog)
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                    21.6%; Score 361; 34.8%; Pred. No. 2.
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Pred. No. 1.3e-11;
1; Mismatches 105
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Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qik protein - chicken

// Alternate names: Qin-induced kinase

C;Species: Gallus gallus (chicken)

C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004

C;Accession: JC7500

C;Accession: JC7500
Neptine/threonine-specific protein kinase (BC 2.7.1.-)
Neptinernate names: protein kinase SNF1 homologs
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #ta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-798 < XIA>
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                                                                                                                                                                                                                                   EYEGPHLDIWSLGVVLYVLVCGSLPFDGPNLPTLRQRVLEGRFRIPYFMSEDCETLIRRM
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                                                                                                                                                           LVVDPTKRITISQIKQHKWMQADPSLRQQ
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                                                                                                                                                                                                                                                                                                               CHSHHIVHRDLKTENLLLDANM-NIKLADFGFGNFYKSGEPLSTWCGSPPYAAPEVFEGK
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Pred. No. 3.4e-11;
0; Mismatches 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                     serine/threonine-specific protein kinase (EC 2.7.1.-) C;Species: Nicotiana tabacum (common tobacco) C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #to C;Accession: A56009
R;Muranaka, T.; Banno, H.; Machida, Y. Mol. Cell Biol. 14, 2958-2965, 1994
                                                                                                                                       A56009
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Characterization

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05-Oct-2004

NPK5

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A; Cross-references: UNIPAC: UPI000009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PI R; Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P. Plant Mol. Biol. 29, 551-565, 1995
A; Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i A; Reference number: $66314; MUID:96123233; PMID:8534852
A; Accession: $6634
A; Reference number: $66314; MUID:96123233; PMID:8534852
A; Molecula type: DNA
A; Residues: 144-198 cfff2>
A; Cross-references: UNIPARC: UPI000009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PI C; Comment: This enzyme plays an important role in a signal transduction cascade regulati C; Genetics:
A; Gene: Akin10; Ak21
A; Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C; Function: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C; Superfamily: SNF1-related protein kinase; protein kinase homology C; Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase F; 25-33/Region: protein kinase Amp-binding mottif F; 48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
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A; Residues: 1-512 < LEG>
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R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis,
Gene 120, 249-254, 1992
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C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,671,42,144/Active site: Lys, Glu, App, Lys #status predicted
F;49,671,451/Binding site: magnesium (Asn, Asp) #status predicted
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A;Accession: A56009
A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; UNIPARC:UPI00000AAD0C; GB:D26602; NID:g496384; PIDN C;Function:
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein. Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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                     EMBL; M27903; AAA60090.1; -; Genomic_DNA.
EMBL; M16750; AAA60089.1; -; mRNA.
EMBL; M54915; AAA36447.1; -; mRNA.
EMBL; M24779; AAA36447.1; -; mRNA.
EMBL; BC020224; AAA91.553.1; -; mRNA.
EMBL; BC020224; AAH20224.1; -; mRNA.
EMBL; AF386792; AAK70871.1; -; Genomic_DNA.
EMBL; AF386792; TVHUP1.
PIR; JU0327; TVHUP1.
PDB; 1XC2; X-Tay; A=14-313.
PDB; 1XR1; X-Tay; A=14-313.
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MEDLINE=88246418; PubMed=2837645;
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ID QST7H7;
PRT; 313 AP
AC QST7H7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
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DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation
DE Pim-1 oncogene (Proviral integration site 1)
GN Name=PIM1; ORFNames=RP3-355M6.1-003;
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Best Local
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PDB; 1Y13; X-ray; A=33-3
PDB; 1Y14; X-ray; A=33-3
PDB; 2B1K; X-ray; B=1-31;
PDB; 2B1K; X-ray; B=1-31;
PDB; 2B1L; X-ray; B=1-31;
Ensembl; ENSGG000137193
HGNC; HGNC:8986; PIM1.
H.INVDB; HIX0005835; -.
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PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
3D-structure; ATP-binding; Kinase; Nuclear
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GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Ser Thr_pkin_AS.
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1YI3; X-ray; A=33-305.

1YI4; X-ray; A=33-305.

2BIK; X-ray; B=1-313.

2BIL; X-ray; B=1-313.

mbl; ENSG00000137193; Homo sapiens
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C: -: CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -:- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AL353579; CAIRO316:1; -; Genomic_DNA.

BR Ensembl; ENSG0000137193; Homo sapiens.

GO; GO:00005724; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004711; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004712; F:protein amino acid phosphorylation; IEA.

INTERPRO; IPR000719; Prot kinase.

Interpro; IPR008271; Ser_Thr_pkinase.

Interpro; IPR008271; Ser_Thr_pkinase.

Interpro; IPR000229; Ser_Thr_pkinase.

Pfam; PF00069; Pkinase; I.

SMART; SM00219; TYC; 1.

R SMART; SM00219; TYC; 1.

R PROSITE; PS00107; PROTEIN KINASE_DOM; 1.

PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

PROSITE; PS00101; PROTEIN KINASE_TOM; 1.

R SMART; SM00220; STOM; 1.

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R PROSITE; PS00101; PROTEIN KINASE, STOM; 1.
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Best Local S
Matches 313
                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
Felinae; Felis.
NUCLEOTIDE SEQUENCE. Fujino Y., Satoh H.,
                                                                                       Pelis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Crani.
Mammalia; Eutheria; Laurasiatheria;
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Mismatches 0;
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R SMR; Q95LJ0; 32-308.

R InterPro; IPR008719; Prot kinase.

R InterPro; IPR008271; Ser_Thr_pkin_AS.

R Pfam; PF00069; Pkinase; 1.

R PfoBom; PD000001; Prot kinase; 1.

R ProDom; PD000001; Prot kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE_DOM; 1.

R PROSITE; PS00118; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

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W AIP-binding; Kinase; Nuclear protein; Nucleotide-binding; PROSED AND PROSED AND PROSED AND PROTEIN KINASE AND PROTEIN KI
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PIM1 BOVIN
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28-FEB-2003
13-SEP-2005
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Name=PIM1;
Bos taurus (Bov
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-i-SUBCELLULAR LOCATION: Cytoplasmic and nuclear-i-PTM: Autophosphorylated (By similarity).
-i-SUMLLARITY: Belongs to the Ser/Thr protein kin-
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ProDom; PD000001; Prot kinase; 1.
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PROSITE; PS50011; PROTEIN KINASE DOW; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding; ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
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-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBCELULUAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- SUBCELULUAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- SIMCELULUAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
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HSSP; Q63450; 1A06.
SMR; Q9N0P9; 32-308.
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                                                                                                  EIHLHSLSPGPSK 313
                                                                                                                                           PFEHDEEIVRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                                                                                                              PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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Proton acceptor (By similarity)
ATP (By similarity).
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SEQUENCE
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Muroidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation updat
Proto-oncogene serine/threonine-protein kin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;

Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X63675; CAA45214.1; -; mRNA
PIR; S26298; S26298.
SMR; P26794; 32-308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawley; TISSUE-Testis; MEDLINE-92319652; PubMed=1620615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P26794;
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InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin
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PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                      ELKLIDFGSGALLKDTVYTDFDGTTVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                             ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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                                               ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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ATP (By similarity).
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Pred. No. 2.3e-112;
6; Mismatches 3;
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RX MEDLING-23389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Garcia B., J., Lu X., Gubbs R.A.,
RA Rathey J., Helton E., Kettemen M., Madan A., Rodrigues S., Sa
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                                                                                                                                                                                Ensembl; ENSMUSG00000024014; Mus musculus. MGI; MGI:97584; Pinl.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity;
GO; GO:0004678; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
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Mammalia; Eutheria; Euarchontoglires;
Muridae; Murinae; Mus.
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oglires; Glires; Rodentia; Sciurognathi;
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; DOI=10.1073/pnas.
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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00111; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nucleotide-binding; Serind/Hy; Kinase; Nucleotide-binding; Serind/Hypropinson; Nucleotide-binding; Serind/Hypropins
Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeo Takahashi K., Ariga H., Iguchi Ariga S.M.M.; "PAPP-1, a novel trayget protein of phosphorylation Eur. J. Biochem. 267:5168-5178(2000).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a -!- SUBUNIT: Binds to RP9
-!- SUBUNIT: Binds to RP9
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear
                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=86272109; PubMed=3015420; DOI=1
Selten G., Cuypers H.T., Boelens W., Ro
Domen J., van Beveren C., Berns A.;
"The primary structure of the putative
homology with protein kinases.";
Cell 46:603-611(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
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                                                                                                                                                    INTERACTION WITH RP9. MEDLINE=20389540; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Pim1; Synonyms=Pim-1; Mus musculus (Mouse).
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SEOUENCE 313 AA; 35451 MW; 1294F16A03B7C7D7
                                                                                                                                                                                                                                                                                                                                                                                                                          Muroidea;
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Euarchontoglires; Glires;
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W., Robanus-Maandag E., Verbeek J.
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RESULT 8
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      28-FEB-2003 (Rel. 41, Created)
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13-SEP-2005 (Rel. 48, Last annotation
Serine/threonine-protein kinase Pim-3
Name=PIM3; Synonyms=PIM-3;
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ACT SITE
BINDING
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InterPro; IPR00871; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_Tom, 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
PROSITE; PS00108; Proto-oncogene; Serine/threonine-protein kinase;
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as long a
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DISEASE: Frequently activated by provirus insertion in murine leukemia virus-induced T-cell lymphomas.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Swiss-Prot entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it as long as its content is in no way modified and this statement is no
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P06803; 32-308
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                                                                                                                                                                    EIHLHSLSPGPSK 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD
                                                                                                                                                                                                                                                                       ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                                                                                                                                                                                            NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL
                                                                                                                                                                                                                                                                                                                                                                                                             MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
                                                                                                                                                       EIHLHSLSPGSSK
                                                                                                                                                                                                                    PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                                                                                                                                                                                                                                                         EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                                                                                                                                            ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG
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44
167
67
313
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                                                                                         STANDARD;
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167
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35537
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(Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1582; D
Pred. No. 2.2e
LO; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
79F4779E9DCBDC16 CRC64;
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                       update)
(EC 2.7.
                                                                                         323
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                          37)
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                       (midb)
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Best Local S
Matches 209
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Oncogene 19:1215-1224(2000).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprote.
-!- PTM: Autophosphorylated.
                                                                                                                                                                                                                                                                                                                                                                                  NP BIND
ACT SITE
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S. TKG; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce as long as its content is in no way modified and this s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria; Aves;
Coturnix.
NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine/threonine-protein kinase; Transferase.
DOMAIN 40 291 Protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ130845; CAB62386.1; -; HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subfamily.
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300
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Pro; IPR008271; Ser thr pkinase
Pro; IPR002290; Ser thr pkinase
Pr00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                               209;
                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                             ILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLN ::|||| |:||| |:||| |:||| |:||| |:|||
                                                                                                                                                                                                                     MLLSKINSLAHLRAAPCNDLHATKLAP--GKEKEPLESQYQVGPLLGSGGFGSVYSGIRV
                                                    DIPFEQDESILRGRLYFRRRISPECQQLIKWCLSLRPSDRPTLEQIFDHQWMHKSEVVKS
                                                                    DIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM-QDVLLPQ
                                                                                                                         RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG
                                                                                                                                                                                                                                      SDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVL
                                                                                                                                                                                                                                                                          MLLSKFGSLAHICSPASMDHLPVKILPPVKVEKEPFDKVÝQVGSVLGSGGFGTVÝAGSRT
| :| | :|
EDCDIRLRTL
                         ETAEIHLHSL
                                                                                                                                                               VMERPELVKDLFDFTTEKGALDEDTARGFFRQVLEAVRHCYGCGVVHRDIKDENLLVDLR
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168
69
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168
69
36597
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                                                                                                                                                                                                                                                                                                                                                                                  Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
; E2A4FA20B6F6396C CRC64;
                                                                                                                                                                                                                                                                                                                                            Score 1140; DB Pred. No. 8e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA.
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RESULT 9
PIM3_HUMAN
ID PIM3_HUMAN

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RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA GBrownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Mozley K.C., Hale S., Farcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schuntz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schuntz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schuntz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
"Consistency checks for characterizing protein forms.";
Comput. Biol. Chem. 27:29-35(2003).
-I- FUNCTION: May be involved in cell cycle progression and appropriate process. Implicated in proliferation of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Aberrant expression of serine/threonine hepatocellular carcinoma development and of human hepatoma cell lines.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q86V86; (Nobertal)
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                 EMBL; AB114795; BAD42438.1; -; EMBL; BC052239; -; NOT_ANNOTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION FROM ESTS.

MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;

Chichester C.. Nikitin F., Ravarini J.-C., Lisacek F.;
                                     HGNC; HGNC:19310; PIM3
InterPro; IPR000719; P:
                                                                                           Ensembl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
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Kaneko S., Mukaida N.
                                                                                                                                                                                                    removed
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Fuji C., Nakamoto Y., Lu P., Tsuneyama
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                                                                                                                                                                                                                                                                                                                                                        Cell lines.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a pinceping.

TISSUE SPECIFICITY: Widely expressed. No expression in conthymus, and small intestine. Expressed in human hepatoma lines but not in normal liver tissues.

TISSUE SPECIFICITY: Widely expressed in human hepatoma times but not in normal liver tissues.
                                                                                                                                                                                                                                                  s Swiss-Prot entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S
                                                                                                                                                                                                                                                                                                             Swiss-Prot
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                                                                                  ENSG00000198355; Homo
IPR000719; Prot_kinase.
IPR008271; Ser_thr_pkin_AS
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                                                                                                                 ANNOTATED_CDS;
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rimates; Catarrhini; Homin
                                                                                                                                                                                                                              modified
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RESULT 10
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

STRAIN-FVB/N; TISSUE-COLON, and Salivary gland;

RX STRAIN-FVB/N; TISSUE-COLON, and Salivary gland;

RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

RA Willaino D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villaino D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 219
                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Euarch---'
Muroidea; Murid---'
NCFT ---
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ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS500108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
ATP-binding; Kinase; Nucleotide-Transferase.
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ACT SITE
BINDING
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                               Serine/threonine-protein
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13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIM3
                                                                                                                                                                                                                                                                                                                                                                                                             Name=Pim3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM
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326
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(Rel. 41,
(Rel. 48,
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Last annotation updat
ein kinase Pim-3 (EC 2
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                                                                                                                                                                                                                                                                                                                                       Mus.
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ATP (By similarity).

Proton acceptor (By

ATP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1133;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
oglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                             update)
(EC 2.7.1.37).
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.6e-75;
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RESULT 11
PIM3_RAT
ID PIM3_AC
O7044
AC 28-FE
DT 28-FE
DT 13-SE
DE Serir
DE Kid-1
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Best Local S
Matches 213
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R SMART; SM00220; S TKC; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS0011; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.

W ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.

T DOMAIN 40 293 Protein kinase.

T DOMAIN 40 293 Protein kinase.

T NP BIND 46 54 ATP (By similarity).

T ACT_SITE 170 170 Proton acceptor (By similarity)

T BINDING 69 69 ATP (By similarity).

SEQUENCE 326 AA; 35970 MW; DD68CBF46354851E CRC64;
PIM3 RAT STANDARD; PRT; 326 AA.
070444;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)
Kid-1) (Kinase induced by depolarization).
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-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phospho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC017621; AAH17621.1; -; mRNA.
EMBL; BC026639; AAH26639.1; -; mRNA.
HSSP; Q03656; 1HOW.
Ensembl; ENSMUSG00000035828; Mus musculus.
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InterPro; IPR000719; Prot kinase.
InterPro; IPR000771; Ser thr pkin AS
InterPro; IPR002290; Ser thr pkinase
Pfam; PF00069; Pkinase; I
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ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
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Pred. No. 4.8e
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                                                                                                                                                                                     Query Match
Best Local S
Matches 213
                                                                                                                                                                                                                                                                                                                            EMBL; AF086624; AAC68900.1; ALT_INIT; mRNA.
EMBL; AF057026; AAC36065.1; -; mRNA.
HSSP; 003656; IHOW.
RGD; 620462; Pim3.
GO; GO:00046774; F:protein serine/threonine ki.
GO; GO:0046777; P:autophosphorylation; IDA.
GO; GO:0016572; P:histone phosphorylation; IDA.
GO; GO:0016572; P:histone phosphorylation; ID.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr_pkinase.
Pfam; PF00069; Pkinase; I.
                                                                                                                                                                                               NP BIND
ACT SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00069; Pkinase, I.

Probom, PD000001; Prot kinase; 1.

SMART; SM00220; S TKC; I.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE TO; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Nuclectide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague-Dawley;
Konietzko U., Kuhl D.;
"Pim-3 is a member of the pim kinase family.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norveĝicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Pim3; Synonyms=Kid1;
                                                                                                                                                                                                                                             Serine/threonine-protein kinase; Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                             Local 213;
                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          including brain.
INDUCTION: By membrane depolarization or forskolin.
PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr protein kinase f
subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s Swiss-Prot entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict as long as its content is in no way modified and this state
119
                    116
                                           60
                                                                 83
                                                                                          _
                                                                                                             سر
                                                                                                                                                  Similarity
                                         MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
            MILSKEGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR
FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV
                                                                                                                                                                                     326
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46
170
                                                                                                                                       Conservative
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54
170
                                                                                                                                                                                     69
36002
                                                                                                                                                 67.6%;
                                                                                                                                                                                     MW;
                                                                                                                                     31;
                                                                                                                                      Score 1128.5;
Pred. No. 5.7e
31; Mismatches
                                                                                                                                                                                               Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
                                                                                                                                                                                      DD6C9BF4635F851E
                                                                                                                                                  .7e-75;
                                                                                                                                                                                                                                                                                                                                                                               IDA.
                                                                                                                                                                                                                                                                                                                                                                                                    kinase
                                                                                                                                                             DB 1;
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unstimulated tissu
                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    activity;
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                                                                                                                                      Gaps
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RESULT OF SUPERIOR SU
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Scheutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
RT and mouse cDNA sequences.";
Br. Droc Narl Asset Ceri II c. 1001.15001.15001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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   Query Match
Best Local S
Matches 213
                                                                                                                                        ProDom; PRO100001; Prot kinase; 1.

ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; TyrKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Hypothetical protein; Kinase; Nucle Serine/threonine-protein kinase; Transferase.

NON TER

1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2005) to the EMBL/GenBan-i-SIMILARITY: Belongs to the Ser/Thr EMBL; BC097317; AAH977317.1 -; mRNA. InterPro; IPR008271; Prot kinase. InterPro; IPR008271; Ser thr pkinase. InterPro; IPR008290; Ser thr pkinase. InterPro; IPR001245; Tyr pkinase. InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4V8M2_RAT
Q4V8M2;
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Mammalia; Eutheria; Euarchontoglires; Glires;
Muroidea; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2005
13-SEP-2005
13-SEP-2005
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                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM
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                                                                                                                  380
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      Conservative
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                                                                                                                     41568 MW;
                              67.6%;
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                              Score 1128.5;
Pred. No. 6.8s
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                                                                                                                  F82BE8E50DD71346
   Mismatches
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annotation update)
                                                                                                                                                                                                    Kinase; Nucleotide-binding
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lires; Rodentia;
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   Indels
                                                         Length
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                                                            380;
7;
Gaps
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Best Local
Matches 21
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01-JUN-2003
01-JUN-2003
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                        116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293
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SMR; Q811X8; Jb-22...

MGI; MGI:1355297; Pim3.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005224; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein amino acid phosphorylation; IEA.

InterPro; IPR000719; Prot_kinase.

R InterPro; IPR008271; Ser_thr_pkin_AS.

RPfam; PF00069; Rkinase; I.

ProDom; PD000001; Prot_kinase; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00103; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

MW ATP-binding; Kinase; Nucleotide-binding;

KW Serine/threonine-protein kinase; Transferase.

Serine/threonine-protein kinase; Transferase.

Serine/threonine-protein kinase; Transferase.

Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2001) to the EMBL/GenBank/DDBJ d-!- SIMILARITY: Belongs to the Ser/Thr protein EMBL; AY026239; AAK16606.1; -; mRNA. HSSP; Q03656; 1Q99.
SMR; Q811X8; 36-292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae; Murinae;
NCBI_TaxID=10090;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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119
                                                                                                                                                                                                                                                             l Similarity
212; Conser
                    FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI
                                                                                                           MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR
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                                                                                    IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG
                                                                                                                                                                        MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Glires; Rodentia; Sciurogna
                                                                                                                                                                                                                                                                             66.8%;
71.9%;
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26,
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2; Mismatches
                                                                                                                                                                                                                                                                               Score 1116;
Pred. No. 4.
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annotation update)
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4.7e-74;
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Best Local S
Matches 205
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NP BIND
ACT SITE
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MOD_RES
                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L29495; AAA85389.1; -; mRNA
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pim-1 proto-oncogene-encoded protein kinase.";
J. Biol. Chem. 272:10514-10521(1997).
-i- CATALYTIC ACTIVITY: ATP + a protein = ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aebersold R., Pelech S.L.; "Identification of the autophosphorylation sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1) NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=PIM3; Synonyms=PIM1;
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subfamily. (Ref.1) called Pim-1 but seems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represent the pim-3 isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swiss-Prot entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179
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                                                                                                                 Similarity
                                            MLLSKINSLAHLRAAPCN-----DLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS
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  MLLSKFGSLAHI ----
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                                                                                             Conservative
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69
4
                                                                                                                                                                                      36964 MW;
                                                                                                                 66.2%;
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  CNPSNMEHLPVKILQPVKVDKEPFEKVYQVGSVVASGGFGTVYS
                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is in no way
                                                                                           Score 1105; Di
Pred. No. 3e-7.
47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA.
                                                                                                                                                                                                                                (partial).
Phosphoserine (by autocatalysis)
Phosphothreonine (by autocatalys
                                                                                                                                                                                                                                                                                                                                Proton acceptor (By similarity).
ATP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                               Protein kinase.
ATP (By similarity)
                                                                                                                                                                                                                                                                                                          Phosphoserine (by
                                                                                                                                                                                        AB4DD61E7A99A38F CRC64;
                                                                                           e 1105; DB 1;
. No. 3e-73;
ismatches 50;
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                                                                                                                                                                                                                                                                                                          autocatalysis)
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RESULT 15

Q66III XENTR
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AMPHILING
AC X CANDUC X
AC X CANDUC X
AC MINITE X
AC X CANDUC X
AC 
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., WcEwan R., Bonaldo M.F., Casaavant T.L., Scheetz T.E.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                        Q66II1_XENTR PRELIMINARY;
   Ensembl; ENSXETG00000009354; Xenopus tropicalis. GO; GO:0005524; F:ATP binding; IEA. GO:0004674; F:protein serine/threonine kinase activity; GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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DR InterPro; IPR008271; Ser_Ehr_pkin_AS.

DR InterPro; IPR008271; Ser_Ehr_pkinase.

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6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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2 US-09-237-543-6

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2 US-09-644-650-4

2 US-09-949-016-7140

2 US-10-10-16-7140

2 US-10-10-10-36-72

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Qy 301 Db 301	Oy 241 Db 241	Qy 181 Db 181	Qy 121 Db 121	Qy 61 Db 61	Qy 1 Db 1	Query Match Best Local Matches 31	RESULT 1 US-09-237-543 Sequence No. Patent No. GENERAL INF APPLICANT: TITLE OF I TITLE OF I TITLE OF I TITLE OF I CURRENT AP CURRENT FI UMBER OP SOFTWARE: SEQ ID NO 8 LENGTH: 3 TYPE: PRT ORGANISM: ORGANISM:		28 29 37 30 31 32 364 33 34 35 35 35 35 35 35 35 35 35 35
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RESULT 2 US-09-644-450-8

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Sequence 9, Application US/09237543A

Patent No. 6143540

GENERAL INFORMATION:

APPLICANT: Kapeller, Rosana

TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 035800/175631

CURRENT APPLICATION NUMBER: US/09/237,543A

CURRENT FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 3313

TYPE: PRT

ORGANISM: Homo sapiens
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TITLE OF INVENTION: NOVEL MOLECULES OF THE HK:
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT FILING DATE: 2000-08-23
INMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 313
TYPE: PRT
ORGANISM: Rattus norvegicus
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Matches 304
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Best Local Similarity
Matches 313; Conserv
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1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
                                                                             Similarity
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                                                                Conservative
                                                                             98.18;
                                                              Score 1636; DB 2;
Pred. No. 3e-161;
6; Mismatches 3;
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                                                                                            Length 313;
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Sequence 9, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
ITITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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RESULT 5
US-08-463-081B-26
; Sequence 26, Application
; Patent No. 5871960
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo
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Best Local Similarity
Matches 304; Conserv
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                                                                                           EIHLHSLSPSPSK 313
                                                                                                                                               PFEHDEBIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEBIQNHPWMQDVLLPQATA 300
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Pred. No. 3e-161;
6; Mismatches
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; TOPOLOGY: n.a
; MOLECULE TYPE:
US-08-463-081B-26
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Best Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/463,0818
FILING DATE: 5-UN-195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
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LENGTH: 313 amino acid
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CORRESPONDENCE ADDRESS:
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ZIP: 90071
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                 EIHLHSLSPSPSK 313
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EIHLHSLSPGPSK 313
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Pred. No. 6.7e-160;
6; Mismatches 5;
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Cell Thereof, and Expression
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Best Local S
Matches 302
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-UNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/330,108; 08/104,736
APPLICATION NUMBER: & 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 30,930
REFERENCE/DOCKET NUMBER: TELEPHONE: (610)470-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Smith, Ker
TITLE OF INVENTION: N
TITLE OF INVENTION: E
TITLE OF INVENTION: E
NUMBER OF SEQUENCES:
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
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ADDRESSEE: (B) STRE
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
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STRANDEDNESS:
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302; Conserv
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     EIHLHSLSPSPSK 313
                                                 PFEHDEEIVKGQVYFRORVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
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Nucleic Acids Encoding CR5 Polypeptide,
Vector and Transformed Cell Thereof, and
Expression Thereof
S: 35
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Pred. No. 6.7e-160;
6; Mismatches 5;
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US-08-462-390B-26
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Best Local Simi
Matches 302;
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GENERAL INFORMATION:
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FILING DATE: 5-UNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECHONE: (610)407-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: n. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 313 amino a TYPE: peptide STRANDEDNESS: n.a.
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                                                                                             ELKLIDFGSGALLKDTVYTDFDGTTVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
                                                                                                                                                  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
                       PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
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96.5%;
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Pred. No. 6.7e-160;
6; Mismatches 5;
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US-08-463-074B-26
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Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, ph. D.
REGISTRATION NUMBER: 90.30
REFERENCE/DOCKET NUMBER: 966 38143
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213,486.32-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 622-7700
TELEFAX: (211) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR1 NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: C
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PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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. (B) STREET:
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Pred. No. 6.7e-160;
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RESULT 9
US-08-465-585C-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 10-NUV-1994
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-NUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 10-NUV-1991
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NUV-1991
ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA AMZe1, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (213) 4894210 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: n. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acid
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Similarity 96.5%;
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                                                                                                         ERPEPVQDLFDF1TERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIL1DLNRG
ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                         ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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. (B) STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1623; DB 2;
Pred. No. 6.7e-160;
6; Mismatches 5;
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US-08-652-446-26
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/46
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/46
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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PRIOR APPLICATION UNMBER: EP APPLICATION NUMBER: EP APPLICATION NUMBER: PCT/UNDBER: PCT/UNDBER: PCT/UNDBER: US OR PRIOR APPLICATION NUMBER: US OR
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                       REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPAX: (213) 489-4210
                                                                                                                                                                                                                                       FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/
                                                                                                                                                                                                                                                                                                                      FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
                                                                                                                                                                                        FILING DATE: 29-OCT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                NAME: Viviana Amzel, REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 5-JUN-
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STATE: California
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: Nucleic Acids Encoding
: Polypeptide, Vector and
: Expression Thereof
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30,930
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TYPE: peptide

STRANDEDNESS: n.a.

TOPOLOGY: n.a.

MOLECULE TYPE: peptide

US-08-652-446-26
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APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF TH
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION UMMBER: US/09/237,543
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 313
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US-09-237-543-7
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; ORGANISM: Mus
US-09-237-543-7
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                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 295; Conserv
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Best Local Similarity
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TYPE: p
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                                            ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
                                                                                                      NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                          ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG
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96.5%; Pred. No. 6.7e-160;
tive 6; Mismatches 5;
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                                                                                                                                                                                                           Score 1584; DB 2;
Pred. No. 7.5e-156;
8; Mismatches 10;
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus r
US-09-644-450-7
                                                                      US-07-857-224B-41
Sequence 41, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
Benner, Steven A.
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Fo.
NUMBER OF SEQUENCES: 114
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US-09-644-450-7
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SEQ ID NO 7
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Best Local Similarity
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TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 03500/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
                                                          CORRESPONDENCE ADDRESS:
STREET:
CITY: Z
STATE:
                             ADDRESSEE: Steven A. Benner STREET: Hadlaubstrasse 151
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                 Zurich
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                                                                                                                                                                                                                                                                                                           PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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94.2%;
                                                                          Predicting Folded Structures
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Pred. No. 7.5e-156;
8; Mismatches 10;
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RESULT 14

US-09-237-543-2
; Sequence 2, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF TH;
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543.
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Best Local S
Matches 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1
TELEFAX: (International) 41 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: (note: this is an international post code COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage COMPUTER: Apple MacIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
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OPERATING SYSTEM: MacIntos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAGES: 42-52
DATE: 1988
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VOLUME: 241
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FILING DATE: 03/25/92
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   NUMBER: US/09/237,543A
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Pred. No. 5.6e-127;
7; Mismatches 3;
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SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
US-09-644-450-2
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US-09-644-450-2
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; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRT
ORGANISM: Homo sapiens
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PATENT NO. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                            Query Match 68.0%; Score 1135; DB 2; Best Local Similarity 69.6%; Pred. No. 3.1e-109; Matches 220; Conservative 34; Mismatches 52;
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Best Local
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CURRENT APPLICATION NUMBER: US/0:
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV
                    FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
                                                               IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG
                                                                                  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR
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Pred. No. 3.1e-109;
Pred. No. 3.2e-109;
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US-10-348-081-13
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Patent No. US20020115120A1
GENERAL INFORMATION:
APPLICANT: Rosanna Kapeller-Liberm
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ALIGNMENTS

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WSLGILLYDMVCGDI 240	ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI	/ 181	Ş
RDIKDENILIDLNRG 180	ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG	0 121	Дb
RDIKDENILIDLNRG 180	ERPEPVQDLFDFTTERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG	/ 121	Ş
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LLDWFERPDSFVLIL 120	NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL	y 61	8
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SGGFGSVYSGIRVAD 60	MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD	7	Ş
th 313; ls 0; Gaps	Match 100.0%; Score 1668; DB 3; Length Local Similarity 100.0%; Pred. No. 5.8e-143; es 313; Conservative 0; Mismatches 0; Indels	Query Match Best Local Sim Matches 313;	
	Rattus norvegicus .8	0	us-
		ച ന	
	FastSEQ for Windows Version 4.0	SOFTWARE:	
	DATE	PRIOR FILI	٠.
	APPLICATION NUMBER: 09/237,543		
	APPLICATION NUMBER: 09/644,450 FILING DATE: 2000-08-23	PRIOR APPL	·. ·.
	FILING DATE: 2001-10-04	CURRENT FI	٠
	FILE REFERENCE: 35800/238856	FILE REFER	
D PROTEIN FAMIL	INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES	TITLE OF I	٠.
	Laura A. kudoiph-Owen Kyle MacBeth	APPLICANT:	
	Tanna Tudy The Discussion	THE PERSON AND ADDRESS OF THE PERSON ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON ADDRESS OF THE PERSON A	

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APPLICANT: GRUENENTHAL GMBH

TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE

FILE REFERENCE: 029310.52818US

CURRENT APPLICATION NUMBER: US/10/705,757

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: CT/EP02/05234

PRIOR APPLICATION NUMBER: DE 101 23 055.9

PRIOR APPLICATION NUMBER: DE 101 23 055.9

PRIOR APPLICATION NUMBER: DE 101 23 055.9

PRIOR FILING DATE: 2001-05-11

NUMBER OF SEQ ID NOS: 11

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 313

TYPE: PRT
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TYPE: PRT
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                                                                                                                                                                                                                                          Sequence 4, Application US/10705757 Publication No. US20040146942A1 GENERAL INFORMATION:
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APPLICANT: TSCHANK, GeOTG
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
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Best Local Similarity
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ORGANISM: Rattus norvegicus
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-791-9
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US-09-971-791-9
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Best Local Sim
Matches 313;
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Best Local Similarity 97.1
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97.1%;
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PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
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Sequence 9, Application US/09971791
; Sequence 9, Application US/09971791
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THE
; FILE REFERENCE: 35800/23856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT APPLICATION NUMBER: 09/444,450
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILLING DATE: 2000-08-23
; PRIOR FILLING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENTY OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THE
; SEQ ID NO 9 1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD Score 1636; DB 3; Pred. No. 4.7e-140; 6; Mismatches 3; DB 3; Length 313; Indels <u>,,</u> Gaps 180 120 120 60 60

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RESULT 6
US-10-394-322A-52
Sequence 52, Application US/10394322A
Publication No. US20030232391A1
Publication No. US20030232391A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUMESIS PHARMACEUTICALS, INC.
APPLICANT: Prescott, John C.
APPLICANT: Prescott, John C.
FILE REFERENCE: 39750-0006 US
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394,322A
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US-10-081-119-18
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US-10-081-119-18
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SEQ ID NO 18
LENCTH: 313
TYPE: PRT
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Best Local
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CURRENT APPLICATION NUMBER: US/10/081,119
CURRENT FILING DATE: 2002-02-21
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APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
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PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
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Local Similarity 97.1%;
les 304; Conservative
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Pred. No. 4.7e-140;
6; Mismatches 3;
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; TYPE: PRT
; ORGANISM: Homo &
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; ORGANISM: Homo
US-10-348-081-13
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APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/10348081 Publication No. US20040038246A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/366,89
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 52
LENGTH: 313
                                                                                                                         Matches 304;
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Best Local
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Best Local
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APPLICANT: MUELLER, Guenter
                                                                                                                                                                                                                                 LENGTH: 313
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                                                                          MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
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                                                            MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD
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                                                                                                                      Score 1636; DB 4;
Pred. No. 4.7e-140;
6; Mismatches 3;
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Pred. No. 4.7e-140;
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PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 1
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-664-421-1
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                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 304; Conserv
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APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
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APPLICANT: IBRAHIM, PRABH
APPLICANT: KUMAR, ABHINAV
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                                                       ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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EIHLHSLSPGPSK 313
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RESULT 9

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Sequence 2, Application US/10705757

Sequence 2, Application US20040146942A1

GENERAL INFORMATION:

APPLICANT: GRUENENTHAL GMBH

FITTLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR

FILE REFERENCE: 029310.52818US

CURRENT APPLICATION NUMBER: US/10/705,757

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: PCT/EP02/05234

PRIOR APPLICATION NUMBER: DE 101

PRIOR FILING DATE: 2001-05-11

INUMBER OF SE0 ID NOS: 11

COCUMBER: DE 101

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Publication No. US20040142864A1

GENERAL INFORMATION:

APPLICANT: BREMER, RYAN

APPLICANT: IBRAHIM, PRABHA

APPLICANT: KUWAR, ABHINAV

APPLICANT: MILBURN, MICHAEL V.

TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE

FILE REFERENCE: 039363/0703

CURRENT APPLICATION NUMBER: US/10/664,421

CURRENT APPLICATION NUMBER: 00/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR FILLING DATE: 2002-09-20

PRIOR FILLING DATE: 2002-09-20

PRIOR FILLING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 60/411,398

PRIOR APPLICATION NUMBER: 60/411,398

PRIOR FILLING DATE: 2002-09-16
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SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 150
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-10-705-757-2
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SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 313
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Similarity 97.1%;
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Pred. No. 4.7e-140;
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APPLICANT: HIRTH, KLAUS-PETER
APPLICANT: MILBURN, MICHAEL VANCE
ITITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
FILE REFERENCE: 03936/0303
CURRENT FILLNG DATE: 2003-012-28
PRIOR APPLICATION NUMBER: 60/437,929
PRIOR FILING DATE: 2003-01-22
PRIOR FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/360,651
PRIOR APPLICATION NUMBER: 60/360,651
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION SUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                    LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-377-268-9
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US-10-377-268-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/10377268 Publication No. US20040171062A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 313
                                                                                                                                                             Matches
                                                                                                                                                                           Query Match
Best Local :
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Matches 304;
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Pred. No. 4.7e-140;
6; Mismatches 3;
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Pred. No. 4.7e-140;
6; Mismatches 3;
                                                                                                                                                                                     Length 313;
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 RESULT 13
US-10-951-406-18
; Sequence 18, Application US/10951406
; Publication No. US20050059630A1
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US-10-951-389-18
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ORGANISM: Homo
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Sequence 18, Application US/10951389
Publication No. US20050058627A1
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as a 7
TITLE OF INVENTION: TTK in Cancer
FILE REFERENCE: 16932.002
CURRENT APPLICATION UNMBER: US/10/951,389
CURRENT APPLICATION UNMBER: US/10/961,389
CURRENT APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: 05/10/081,119
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
TYDE: DET
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EIHLHSLSPSPSK
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Pred. No. 4.7e-140;
6; Mismatches 3;
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PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR PILING DATE: 2004-09-19
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
Type: Dom
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APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic TITLE OF INVENTION: Target in Cancer FILE REFERENCE: 16932.002
CURRENT APPLICATION NUMBER: US/10/951,406
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
TYPE: PRT
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Publication No. US20050063974A1
GENERAL INFORMATION:
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Best Local :
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APPLICANT: Jefferson, Anne B.
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic TITLE OF INVENTION: Target in Cancer FILE REFERENCE: 16932.002
CURRENT APPLICATION NUMBER: US/10/951,477
CURRENT FILING DATE: 2004-09-27
CURRENT FILING DATE: 2004-09-27
TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 4.7e-140;
6; Mismatches 3;
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PRIOR APPLICATION NUMBER: 10/081,119
PRIOR FILING DATE: 2002-02-21
PRIOR PELLING DATE: 2001-02-21
PRIOR PELLING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 10/360,848
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 09/570,593
PRIOR APPLICATION NUMBER: 09/134,112
PRIOR PELLING DATE: 2000-05-14
PRIOR PELLING DATE: 1099-05-14
PRIOR APPLICATION NUMBER: 10/63,692
PRIOR PELLING DATE: 2000-07-25
PRIOR PELLING DATE: 2000-07-25
PRIOR PELLING DATE: 2000-07-25
PRIOR PELLING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/148,936
PRIOR APPLICATION NUMBER: 60/148,612
PRIOR APPLICATION NUMBER: 60/145,612
PRIOR APPLICATION NUMBER: 10/698,959
PRIOR APPLICATION NUMBER: 10/698,959
PRIOR APPLICATION DATE: 1990-07-26
PRIOR PELLING DATE: 1990-07-26
PRIOR APPLICATION NUMBER: 10/698,959
PRIOR APPLICATION NUMBER: 10/698,959
PRIOR APPLICATION DATE: 10/698,959
PRIOR APPLICATION DATE: 2003-10-30
Remaining Prior Application data removed - See
NUMBER OF SEQ ID NOS: 84
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US-10-977-087-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Vivian W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Ap
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kennedy, Giulia C.
APPLICANT: Khoja, Hamiduddin
APPLICANT: Shyamala, Venkatakrishna
APPLICANT: Shyamala, Venkatakrishna
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
TITLE OF INVENTION: AND THEIR METHODS OF USE V
FILE REFERENCE: 2300-21986
CURRENT APPLICATION NUMBER: US/10/977,087
CURRENT FILING DATE: 2004-10-28
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Chan, Vivien W.
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Xin, Giulia C.
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No. US20050130926A1
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Pred. No. 4.7e-140;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-087-18
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                                                                                                                                    EIHLHSLSPSPSK 313
                               PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
                                                                ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
                                                                                                   ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
EIHLHSLSPGPSK 313
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Search completed: May 4, 2006, 05:32:06 Job time : 92.6667 secs

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1: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep1:*

2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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9: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

10: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

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12: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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8 US-10-511-937-2982
9 US-10-501-841-40
11 US-11-103-065-2
11 US-11-103-065-2
11 US-11-087-099-9816
12 US-11-087-099-9816
13 US-11-087-099-11500
14 US-11-113-424-118
14 US-11-113-424-118
15 US-11-1087-099-12331
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944.812 Million cell updates/sec
                              Sequence 373, App
Sequence 2982, Ap
Sequence 32, Appl
Sequence 40, Appl
Sequence 690, Appl
Sequence 74, Appl
Sequence 74, Appl
Sequence 115, Appl
Sequence 11, Appl
Sequence 11500, A
Sequence 1231, Appl
Sequence 1231, Appl
Sequence 1231, Appl
Sequence 3611, Appl
Sequence 397, Appl
Sequence 397, Appl
Sequence 391, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 22124, A
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; SEQ ID NO 373 ; LENGTH: 455 ; TYPE: PRT ; ORGANISM: rat ; ORGANISM: rat

RESULT 1 US-10-784-00 Sequence 3 Publicatio GENERAL IN APPLICANT TITLE OF FILE REFE CURRENT A CURRENT A CURRENT A NUMBER OF SOFTWARE:			44		41	40	39	38	37	36	35	34	33	32	<u>۵</u> 1	30	29	28	27	26	25	24	23	22	
SULT 1 SulT 1 Sequence 373, Application US/10784004 Publication No. US20060084066A1 GENERAL INFORMATION: APPLICANT: Biogen Idec TITLE OF INVENTION: Surrogate Marker FILE REFERENCE: 08201.6029-00000 CURRENT APPLICATION NUMBER: US/10/78 CURRENT FILING DATE: 2004-02-20 NUMBER OF SEQ ID NOS: 1251 SOFTWARE: PatentIn version 3.2		322.5			3 C 3 C 5 C	N	325.5	327	329.5	331.5	332	333.5	334.5	335.5	336.5	သ (၁)	ယ ယ (၁၈	338	338	338	338.5	•	340.5	342.5	
104-373 373, Application U 373, Application U 373, Application U NFORMATION: UT: Biogen Idec 'INVENTION: Surrog PERENCE: 08201 6029 APPLICATION NUMBER FILING DATE: 2004 P SEQ ID NOS: 1251 P: PatentIn version		19.3	19.3	. ٥	ی م	19.5	9	9.6	9.8	9.9	9.9	0.0	0.1	.1	0.2	0	20.3				0			20.5	
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ULT 1 10-784-004-373 equence 373, Application US/10784004 ublication No. US20060084066A1 ENERAL INFORMATION: APPLICANT: Biogen Idec TITLE OF INVENTION: Surrogate Markers of Pain FILE REFERENCE: 08201.6029-00000 CURRENT APPLICATION NUMBER: US/10/784,004 CURRENT FILING DATE: 2004-02-20 NUMBER OF SEQ ID NOS: 1251 SOFTWARE: PatentIn version 3.2	ALIGNMENTS	US-10-370-959-31		US-11-087-099-8358	US-11-151-601-4	US-11-096-568A-20430	US-11-096-568A-20431	US-11-087-099-1845	US-11-096-568A-18364		US-11-087-099-3898	رن ت	US-11-087-099-1886	0-204-639-17	US-11-096-568A-32575	US-10-995-561-877	US-10-995-561-876	US-10-995-561-880	US-10-995-561-878	US-10-995-561-881	11-087-099-	US-11-177-138-10	10-770-726-6	US-10-784-004-951	
		31,	17. App	Sequence 8358, Ap		Sequence 20430, A			Sequence 18364, A	i, Appl	Sequence 3898, Ap	Sequence 65, Appl	Sequence 1886, Ap	.7, Appl	e 3251		876	880.	878,	881	۲,	e 10,	67, F	Sequence 951, App	

Query Match 67.8%; Score 1131.5; D) Best Local Similarity 72.5%; Pred. No. 3e-89; Matches 214; Conservative 30; Mismatches 368 236 308 176 248 116 189 130 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR 50 VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115 1 MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLBAVRHCHNCGVLHRDIKDENILI IADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM FLIVLERPEPAQUIFDFTTERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV DB 9; 44; Indels Length 455; 7; Gaps 290 422 175 188 235 307 247 σ

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RESULT 2

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APPLICANT: MORYIS, MacDonald
APPLICANT: ROSENBERG, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION UMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
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Publication No. US20060088836A1
GENERAL INFORMATION:
                                                                                                      Sequence 32, Application US/10501841
Publication No. US20060084055A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
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SEQ ID NO 2982
LENGTH: 334
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Best Local Similarity 55.9
Matches 170; Conservative
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APPLICANT:
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ORGANISM: Homo sapiens
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Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
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Wang, Aijun
                                                                     Mannion, Jane
Clapper, Jonathan David
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Prentice, James
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Fry, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.1%; Score 869; DB 8; Length 334; 55.9%; Pred. No. 6.5e-67; tive 43; Mismatches 73; Indels
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Ordonez, Nadia
APPLICANT: Ortonez, Nadia
APPLICANT: Cortex Corporation
APPLICANT: Cortex Corporation
APPLICANT: Corixa Corporation
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
APPLICANTON NUMBER: US/10/501,841
CURRENT FILING DATE: 2002-07-14
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
NUMBER: OF SEG ID NOS: 124
SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: and Therapy of Hematological Malignancies
FILE REFERENCE: 014058-014402PC
CURRENT APPLICATION NUMBER: US/10/501,841
CURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 10/057,475
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2003-01-22
INUMBER OF SEG ID NOS: 124
SOFTWARE: Patentin Ver. 2.1
SEG ID NO 32
LENGTH: 334
TYPE: PRT
ORGANIAM: Homo sapiens
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US-10-501-841-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 VYSPPEWIRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIVKGQVYFRQRVSSECQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 NGQK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 LİRRCLAPKPSSRPSLEEILLDPWMQTPAEDVTPQPLQRRPCPFGLVLATLSLAWPGLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10501841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73; Indels
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US-11-103-065-2
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TITLE OF INVENTION: 2150, Human Protein Kinase Far
ITITLE OF INVENTION: Member and Uses Therefor
FILE REFERENCE: MPI2001-137P1RNM
CURRENT APPLICATION NUMBER: US/11/103,065
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR APPLICATION NUMBER: 00/301,702
PRIOR FILING DATE: 2002-06-27
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 7
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Best Local S
Matches 166
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ
SEQ ID NO 2
LENGTH: 311
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                       Local Similarity
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Local Similarity 58.0%;
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                                                                 SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTR 205
                                                                                                                                                                                                                                GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLFVAIKHVEKDRISDWGELPNGTRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR 145
                  VYSPPEWIRYHGYSAAVWSLGILLYDMVCGDIPFEHDEBIVKGQVYFRQRVSSECQH 265
                                                                                                                                        LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR
                                                                                                                                                                            MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATAEIHLHSLSPSP 311
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VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA
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                                                                                                                                                                                                                                                                                                     51.9%;
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; Pred. No. 9.7e-67;
41; Mismatches 74
                                                                                                                                                                                                                                                                                     Score 866.5; DB 11;
Pred. No. 9.7e-67;
1; Mismatches 74;
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                                                                                                                                                                                                                                                                                       Indels
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Sequence 690, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: Patentin 3.2

INVENTE: 620
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US-10-877-346-74
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Publication No. US20060014153A1
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
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APPLICANT:
APPLICANT:
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Best Local Similarity
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APPLICANT:
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APPLICANT:
APPLICANT:
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                APPLICANT:
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 LIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATAEIHLHSLSPSP
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I: Shimkets, Richard A
INVENTION: Novel Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                                                                                                                                                                                                                                                                                                       QHLIRWCLSLRPSDRPSFEEIQNHPWM 290
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                                Kekuda, Ramesh
Spytek, Kimberly
Leach, Martin D
                                                                                                                                                                                                                                                                                                                                                                                                                   RGLIRWMLMVNPDRRATIEDIANHWWV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEWIRYHRYHGRSAAVWSLGILLYDMVCGDIP---FEHD---EEIVKGQVYFRQRVSSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHNLKHRYELQETLGKGTYGKVKRATERFSGRVVAIKSIRKDKIKDEQDM----VHIRREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEIVNGRPYRGPEVDSWALGVLLYTLVYGTMPFDGFDHKNLIRQISSGE-YREPTQPSDA
                                                                                                                                 Ellerman, Karen
Grosse, William M
Alsobrook II, John P
                                                                                                                                                                                                      Millet, Isabo
Stone, David
                                                                                                                                                                                                                                      Smithson,
                                                                                                   Lepley, Denise M
Burgess, Catherine
                                                                                                                                                                                       Gunther, Erik
                                                                                  Padigaru, Muralidhara
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                                                                                                                                                                                                                        on, Glennda
Isabelle
                                                Kimberly A
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RESULT 8
US-11-087-099-9816
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CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/964,956
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PRILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR PILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR PILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR PILLING DATE: 2000-09-28
PRIOR PILLING DATE: 2000-09-28
PRIOR PILLING DATE: 2000-09-28
PRIOR PILLING DATE: 2000-09-28
PRIOR PILLING DATE: 2000-10-03
PRIOR PILLING DATE: 2000-10-05
PRIOR FILLING DATE: 2000-10-05
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEG ID NOS: 12464
SEQ ID NO 9816
LENGTH: 504
                                                                                                                                                                             Sequence 9816, Application US/11087099 Publication No. US20060041961A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 96; Conserv
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Publication No.
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; ORGANISM: Cucumis sativus 
US-11-087-099-9816
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN '
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN '
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REFERENCE: DO185 PCT
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US 60/350,061
PRIOR APPLICATION NUMBER: US 60/350,061
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
NUMBER OF SEQ ID NOS: 795
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SEQ ID NO 357
LENGTH: 950
TYPE: PRT
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Best Local Similarity
Matches 90; Conserv
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Best Local Similarity
Matches 87; Conserv
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LVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQ
                                                   LSLRPSDRPSFEEIQNHPWM-----QDVLLPQ
                                                                                                       OYEGPOLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRIPYFMSEDCEHLIRRM
                                                                                                                                                           RYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIVKGQVYFRQRVSSECQHLIRWC
                                                                                                                                                                                                                     CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEGQ
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31.8%; Pred. No. 2.5e-23;
tive 52; Mismatches 113
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Pred. No. 1.1e-23;
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US-11-087-099-11500
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US-11-241-056-11
                                                                                                                     ; ORGANISM: Lycopersicon esculentum US-11-087-099-11500
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                                                                                                                                                                         APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 11500
LENGTH: 514
                                                                                                                                                                                                                                                                                                                                                      Sequence 11500, Application US/11087099
Publication No. US20060041961A1
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SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 631
                                                                            Query Match
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                                       Matches
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TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-US
CURRENT APPLICATION NUMBER: US/11/241,056
CURRENT FILING DATE: 2005-09-30
PRIOR APPLICATION NUMBER: US/09/980,464
PRIOR FILING DATE: 2001-11-27
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                                     Local Similarity les 87; Conserv
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38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPE 124
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                                       Conservative
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                                21.5%; Score 358; DB 11; 33.2%; Pred. No. 6.8e-23; tive 54; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
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Pred. No. 2.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 116;
                                     105;
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                                                                        Length 514;
                                     Indels
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                                   Gaps
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RESULT 12
US-10-877-346-72
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                                SOFTWARE: PatentIn Ver.
SEQ ID NO 72
LENGTH: 256
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR ELING DATE: 2004-06-25

PRIOR ELING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR ADDITION NUMBER: US/09/964,956
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PRIOR
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
                                                                                                  Remaining Prior Applic
                                                                                                                                  PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-10-05
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CURRENT FILING DATE: 2004-06-25
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TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding
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ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                        APPLICATION NUMBER: 60/237,434 FILING DATE: 2000-10-03
                                                                                                                                                                                                                           APPLICATION NUMBER: 60/236,135
                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/236,066 FILING DATE: 2000-09-27
                                                                                                                                                                                                           FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              FILING DATE: 2000-09-
                                                                                                                                                                                                                                                                                                                 FILING DATE:
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Smithson, Glennda
Millet, Isabelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellerman, Karen
Grosse, William M
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                                                                                                                    Application data removed
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Kimberly A
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; OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: sequence US-11-113-424-183
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OTHER INFORMATION: Serine/Threoniune protein kinase Cor
OTHER INFORMATION: Sequence
US-10-877-346-72
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US-11-113-424-183
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publication No. US20050260713A1
GENERAL INFORMATION:
APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids
FILE REFERENCE: 21402-225
CURRENT APPLICATION UMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 183
              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
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PRIOR APPLICATION NUMBER: 60/288,153
PRIOR FILING DATE: 2001-05-02
                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                       FEATURE:
                                                                                                                                                                       LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/307,506 FILING DATE: 2001-07-24
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/315,617 FILING DATE: 2001-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/257,314
FILING DATE: 2000-12-20
APPLICATION NUMBER: 60/311,613
FILING DATE: 2001-08-10
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21.3%; Score 355.5; DB
33.0%; Pred. No. 4.7e-23
tive 56; Mismatches 9
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Pred. No. 4.7e-23;
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TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 12331
LENGTH: 504
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les 98; Conserv
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                                                                                                                                                                                                                                    139 LQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVY 198
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                                                                                                 QVY-FRQRVSSECQHLIRWCLSLRPSDRPSFEEEIQNHPWMQDVL----LPQATAEIHLH 305
                                                                                                                                     LKTSCGSPNYAAPEVVSGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKS
                                                                                                                                                                                                        -KTPDMEEKLRREIKICRLFVHPHVIRLYEVIETPTDIYVVMEYVKS-GELFDYIVEKGR 111
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ilarity 32.5%;
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Pred. No. 2.9e-22;
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RESULT 15
US-11-087-099-3997
; Sequence 3997, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

APPLICANT: Abad, Mark S.

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Search completed: May 4, Job time: 16.3333 secs
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                                                                                                                                                                                                                                                                                                                                   Query Match 21.0%; Score 350; DB 11; Length 512; Best Local Similarity 31.7%; Pred. No. 3.3e-22; Matches 84; Conservative 60; Mismatches 99; Indels 22;
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                                                    248 IPRMLIVDPMKRMTIPEIRLHPWFQ 272
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                                                                                                                                                                                                                                                                                               38 YQVGPLLGSGGFGSVYSGIRVADNL----PVAIKHVEKDRISDWGELPNGTRVPMEVVLL 93
                                                                                                        IRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIVKGQVYFRQRVSSBCQHL 266
                                                                          IRWCLSLRPSDRPSFEEIQNHPWMQ 291
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Human PIM	Human cal	Human pro	Human ser	Human HKI	Human ser	Plant ful	нwннJ20 р	Colurnix	Human pro	Human kin	Rat prote	PIM1 domi	Mouse Pim	House mou	Mouse Pim	Mus muscu	Murine Pi	Mouse ser	Murine PI	Mouse pro

ALIGNMENTS

RESULT 1
ABG33016
ID ABG3
XX ABG3
XX ABG3
XX ABG3
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XX ACUL
KW HKII
KW Giff
KW Walc
XX The
PF 04-(
PF 23-1
XX Modi
PT Ser
YX Modi
PT Ser
CCC hum
CC Sup
CC Linv
CC inv HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoietic neoplastic disorder; Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML; ABG33016 standard; protein; 313 26-JAN-1999; 99US-00237543. 23-AUG-2000; 2000US-00644450. 04-OCT-2001; 2001US-00971791. Rattus norvegicus. Waldenstrom's macroglobulinaemia; Rat protein kinase phosphorylation site ABG33016; Kapeller-Libermann R, 22-AUG-2002 US2002115120-A1 20-DEC-2002 (MILL-) MILLENNIUM PHARM INC. (first entry) Rudolph-Owen LA, ₿ ΨM ; #2 Macbeth

Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide. Example 3; Page 39-40; 48pp; English.

WPI; 2002-712471/77.

The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method is useful for modulating the level or activity of HKID-1 polypeptide or polypucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or

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RESULT 2
AAA019789
ID AAO1
XX AAO1
DT 11-J
XX Rat
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The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with
                                                                           Claim 1;
                                                                                                                   Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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DB; ABZ69187.
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RESULT 3
ABR62938
ID ABR66
XX ABR66
XX ABR6
XX Rat;
XX Rat;
XX Rat;
XX Rat;
XX PA
DE Rat
DE Rat
DE Rat
DE Rat
CX Rat
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CX Rat
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Best Local S
Matches 313
 The present sequence is the protein sequence of protein kinase and proto-oncogene, PIM-1. PIM-1 paralogues of novel human and murine PIM-3 prote
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                                                                          New human or murine PIM-3 DNAs or po
agent for identifying anti-type 2 di
treating insulin resistance or type
                                                                                                                                                                               (AVET
                                                                                                                                                                                                                                                                                                           Rattus norvegicus.
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                                                                                                                                                         Mueller
                                                   Page 39; 40pp;
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Pred. No. 9.6e-159;
Mismatches 0;
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                                                                          polypeptides, useful for
diabetes mellitus drugs,
pe 2 diabetes mellitus.
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ce of the rat serine/threonine PIM-1 proteins are the proteins (see ABR62932 and
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RESULT 4
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ID AEB8
XX AEB8
XX AEB8
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XX MIM
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Best Local Similarity
Matches 313; Conserv
WPI; 2005-556609/57.
N-PSDB; AEB96038.
REFSEQ; NP_058730.
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                                                                                                                                                                                                                                                                        30-JAN-2004; 2004DE-10004894
                                                                                                                                                                                                                     30-JAN-2004; 2004DE-10004894
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protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rat PIM-1 serine-threonine kinase
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                                                                                                                                                                GRUENENTHAL GMBH
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serine-threonine kina
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Pred. No. 9.6e-159;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uropathic; gene therapy;
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Identifying substances that regulate PIM kinases, useful for treatment and diagnosis of urinary incontinence and the urge to urinate, and similar use of PIM proteins or nucleic acids.
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Claim ۲. 10; 37pp;

regulate urinary incontinence and the urge to urinate. The method comprises incubating a test compound with a cell and/or cell preparation that has synthesized a specific protein of the PIM (proviral integration site) kinase family and measuring either binding of the test compound to the PIM kinase, or a functional parameter that is altered by the binding. The method of the invention demonstrates uropathic and gene therapy applications and may be useful for treatment and diagnosis of urinary incontinence and the urge to urinate. The method is based upon regulating the activity or expression of PIM kinases that are involved in bladder control. The current sequence is that of the Norway rat PIM-1 serinethreonine kinase protein of the invention.

Sequence 313 Ā

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Best Local :
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                        EIHLHSLSPSPSK
                                                                 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
                                                                                                                 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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EIHLHSLSPSPSK
                                               PFEHDEETVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEETQNHPWMQDVLLPQATA
                                                                                                    ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                       ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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                                                                                                                                                                                                                                                                                                            100.0%; Score 1668; llarity 100.0%; Pred. No. 9. Conservative 0; Mismatches
313
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}.6e-159;
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ABP54943 standard; protein; 313

ABP54943;

13-JAN-2003 (first entry

Human Pim1.

RESULT 5
ABB54943
ID ABB95
XX ABB969
XX ABB95
XX ABB95
XX Y Huma
XX Pinl
KW Pinl
KW Wnitc
KW huma
XX Homo
XX W Homo
XX W Homo
XX W WO20
XX WO20
XX WO21
XX WO21
XX Y Z1-F Pim1; tyrosine threonine mitotic checkpoint; color human; gene therapy. colon kinase; TTK; protein cancer; tumo enzyme;

Homo sapiens.

WO200268444-A1

06-SEP-2002.

21-FEB-2002; 2002WO-US005278

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RESULT 6
ABG33017
ID ABG3
XX
AC ABG3
AC ABG3
XX
AC ABG3
XX
AC HUma
XX
Huma
XX
KW HKIE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abnormal expression levels a prostate and ovarian cancer.
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   HKID-1; serine/threonine kinase; cellular proliferative disorder;
                                                             Human protein kinase phosphorylation site
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(TTK) activity, useful in diagnosing and treating disorders with
all expression levels and activity of TTK, such as lung, colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Pred. No. 1.6e-155;
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Best Local S
Matches 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method is useful for modulating the level or activity of HKID-1 polypeptide or polynucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or differentiative disorders including cancer or haematopoietic neoplastic disorders e.g. Acute promyeloid leukaemia (APMI), Chronic myelogenous leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the amino acid sequence of a human protein kinase phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differentiative disorder; cancer; Acute promyeloid leukaemia; APML; Waldenstrom's macroglobulinaemia;
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23-AUG-2000; 2000US-00644450
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                                                                                    PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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)B; ABZ69186.
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with an amount of an agent effective to reduce TTK polypeptide activity of growth of a cancerous cell (comprising: (i) detecting the activity of a cylpeptide in the presence of a candidate agent (ii) comparing the activity of a cylpeptide in the presence of a candidate agent (ii) comparing the activity of TTK polypeptide in the presence of a candidate agent (ii) comparing the activity of TTK polypeptide activity in the absence of the candidate agent; and (ii) comparing the activity to TTK polypeptide activity in the absence of the candidate agent; and (ii) comparing the contacting a cancerous cell displaying elevated expression of a TTK-contacting polymucleotide with a candidate agent; and (ii) determining the prognosis of a cancerous disease other than ovarian cancer in a control non-concer (comprising: (i) detecting expression of TTK polypeptide activity) and assessing the prognosis of a cancerous disease other than ovarian cancer in a control non-cancer cell, where the level of expression of TTK in the test cancer cell with a level of expression of the polymucleotide in the test cancer cell with a level of expression of the polymucleotide in a control non-cancer cell is condicative to the level of expression in the control non-cancer cell is condicative of the prognosis of the cancerous disease). The methods are custoff of a cancerous disease other than cancer that cancer cell, identifying a candidate agent that reduces TTK condicativity and assessing the prognosis of a cancerous disease other than cancer. The methods are also useful for determining the ability of a subject to respond to a particular therapy e.g. as a basis of control not one of the cancerous activity and assessing the ability of a subject to respond to a particular therapy e.g. as a basis of control not of the cancerous activity and assessing the ability of a cancer to the present sequence represents a closely related to pretein to human TTK. In this case human TMM and the defined)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or polynucleotide in a test cell obtained from the subject and in a normal non-cancer cell, where an increase in the expression level of TTK protein or nucleic acid in the test cell compared to that in the normal cell, indicates the presence of cancer other than ovarian cancer. Also included are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell are reducing growth of a cancerous cell are reducing growth of a cancerous cell (by contacting a cancerous cell are reducing growth of a cancerous cell are reducing growth or a cancerous cell are reducing growth
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) JEFFERSON A
) CHAN V W.
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The present sequence is the protein sequence of the human serine/threonine protein kinase and prote-oncogene, PIM-1. PIM-1 proteins are the paralogues of novel human and murine PIM-3 proteins (see ABR62932 and ABR62933) of the invention, which are therefore expected to be involved in cancer and cell growth regulation. PIM-3 is also involved in the development of insulin resistance and type 2 diabetes mellitus. The invention relates to the use of PIM-3 nucleic acids and proteins in: screening assays for compounds that modulate insulin resistance or type 2
                                                                                                                                                                                                                                                                               New human or murine PIM-3 DNAs or polypeptides, useful for agent for identifying anti-type 2 diabetes mellitus drugs, treating insulin resistance or type 2 diabetes mellitus.
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                                                                                                                                                                                                                                 Example 2; Page 40; 40pp; English.
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Pred. No. 1.6e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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Pred. No. 1.6e
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New composition comprising

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RESULT 11
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Pred. No. 1.6e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
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     EIHLHSLSPGPSK
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                                                                                                                  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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97.1%;
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Pred. No. 1.6e-155;
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                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain Barre syndrome and chronic inflammatory demyelinating polypeptide of the polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome;
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               ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligase, etc. The present sequence is the human PIM 1 protein. This sequence is used to illustrate the method of invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Designing a ligand binding to a target molecule, comprises identifying molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesizing ligand.
                                                                                                                                                                                                                                                                                                                                      Sequence
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16-SEP-2002; 2002US-0411394P.
20-SEP-2002; 2002US-0412341P.
02-JAN-2003; 2003US-0437929P.
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Pred. No. 1.6e
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RESULT 14
ADP24227
ID ADP24
XX ADP24
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XX ADP24
XX PRO.p
XX
cc antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, cc osteopathic, antidiabetic, dermatological, antigratic, antiallergic, cc antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide cof the invention may have a use in gene therapy. The PRO polypeptide, its copypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, cc juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy. Sjogren's syndrome, systemic croaditis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune crombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, ademyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, ca chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis, scleronin, scleronin, primary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7;
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RESULT 15
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Best Local Simi
Matches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urricaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein of the invention.
                      WPI; 2004-748778/73.
N-PSDB; ADT07366.
                                                                                                       03-APR-2003;
                                                                                                                               05-APR-2004; 2004WO-JP004917
                                                                                                                                                       21-OCT-2004
                                                                                                                                                                                                                                                                              Human protein
                                                                                                                                                                                                                                                                                                                             ADT07365
                                                        Kobayashi M,
                                                                                                                                                                              WO2004090158-A1
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                          anticancer
                                                                                                                                                                                                                                                   Prophylactic-therapeutic agent; apoptosis
                                                                                                                                                                                                                                                                                                      13-JAN-2005
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97.1%;
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Pred. No. 1.6e-155;
6; Mismatches 3;
                                                                                                                                                                                                                                                                              anticancer
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                                                                                                                                                                                                                                         kinase
                                                                                                                                                                                                                                       inducing agent;
Pim-1; cancer;
                                                                                                                                                                                                                                                                           compound screening method
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Screening

for a prophylactic-therapeutic apoptosis inducing agent

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Search completed: May 4, 2006, 05:24:47 Job time: 114.667 secs
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Best Local Similarity
Matches 304; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of screening a prophylactic-therapeutic agent for an apoptosis inducing agent or an enhancer of an anticancer agent. The method involves the use of a serine/threonine kinase Pim-1, its partial peptide or its salt. Also disclosed is a kit for carrying out the method of the invention. The method is useful for screening a prophylactic-therapeutic agent for cancer. The method is also useful for prophylactis and/or treatment of cancer, inducing apoptosis, treating a patient having a solid tumour that is resistant to an anticancer agent (induced by hypoxia), and for screening a substance that promotes or inhibits the activity of serine/threonine kinase Pim-1. The present sequence represents a human polypeptide relating to the present invention.
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ilarity 97.1%;
Conservative
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Pred. No. 1.6e-155;
6; Mismatches 3;
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ALIGNMENTS

R;Wingett, D.; Reeves, R.; Magnuson, N.S.
Nucleic Acids Res. 20, 3183-3189, 1992
A;Title: Characterization of the testes-specific pim-1 transcript in A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Accession: S26298 C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; p F;36-290/Domain: protein kinase homology <KIN>F;44-52/Region: protein kinase ATP-binding motif F;67/Active site: Lys #status predicted A;Experimental source: testis
A;Note: testis-specific transcript is shorter and more stable than the somatic transcriC;Comment: Pim-1 autophosphorylates at unknown sites. protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S26298 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon, A;Note: in testis may be involved in signal transduction events of normal germ cell mat A; Molecule type: mRNA A; Residues: 1-313 <WIN> C; Function: A;Cross-references: UNIPROT:P26794; UNIPARC:UPI0000131AD6; EMBL:X63675; NID:g56902; PIL Matches Query Match Local 301 241 241 181 181 121 al Similarity 313; Conserv 121 61 61 \vdash 1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD ERPEPVQDLFDFITERGALQEBLARSFFWQVLBAVRHCHNCGVLHRDIKDENILIDLNRG NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL EIHLHSLSPSPSK 313 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWWQDVLLPQATA ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHGRSAAVWSLGILLYDMVCGDI ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA Conservative 100.0%; Scc y 100.0%; Pre Score 1668; DB 1; Pred. No. 2.6e-74; Length 313; Indels 0; Gaps proto-oncoger 300 180 120 300 240 180 120 60 240 60 0 pro

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A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F;36-290;Domain: protein kinase homology <KIN> P;44-52/Region: protein kinase ATP-binding motif F;67/Active site: Lys #status predicted
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A;Cross-references: GDB:119495; OMIM:164960
A;Cross-references: GDB:119495; OMIM:164960
A;Map position: 6p21.2-6p21.2
A:Introns: 28/2; 63/3; 80/3; 203/1; 262/1
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A;Residues: 1-14,'RA,'17-313 <ZAK>
A;Residues: 1-14,'RA,'17-313 <ZAK>
A;Residues: 1-14,'RA,'17-313 <ZAK>
A;Residues: 1-14,'RA,'17-313 <ZAK>
A;Residues: 1-10,'RA,'17-313 <ZAK-
A;Pomen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immu A;Reference number: 158412; MUID:88217305; PMID:3329709
A;Accession: 158412
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A;Title: The cDNA sequence and gene analysis A;Reference number: A27476; MUID:87277423; PN A;Accession: A27476
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A;Residues: 1-313 <REE>
A;Residues: 1-313 <REE>
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI0000001060;
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI0000001060;
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A;Title: Primary Structure of the putative human oncogene,
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327
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A; Residues: 1-313 < DOM>
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J. Cell. Biochem. 35, 105-112, 1987
A;Title: Cloning and characterization of the human PIM-1 gene: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 31-Mar-1999 #sequence_revision 07-Oct-1994 #text_change
C;Accession: JU0327; A46554; A27476; I58412
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
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                                ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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  ERPEPVQDLFDF1TERGALQEELARSFFWQVLEAVRHCHNCGVLHRD1KDEN1L1DLNRG
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RESULT S55333

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pim-2

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mouse

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A;Accession: A24169
A;Cross-references: UNIFROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:g20
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Function:
C;Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Superfamily: protein kinase homology <KIN>
F;36-29/Domain: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted
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A;Title: The primary structure of the putative oncogene A;Reference number: A24169; MUID:86272109; PMID:3015420
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C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
R;Selten, G; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase (EC 2.7.1.37) pim-1 - mouse N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene
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A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonir
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;99-345/Domain: protein kinase homology <KIN>
F;99-105/Region: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted
submitted to the EMBL Data A; Reference number: Z19538 A; Accession: T2255 A; Status: preliminary; tran A; Molecule type: DNA
                                                                                         hypothetical protein F45H7.4 - Caenorha C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision C;Accession: T22255 #S.Percy, C.
                                                                                                                                                                                             RESULT
T22255
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C;Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change
C;Accession: S5533; A43093; B43093
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; v
EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking th
A;Reference number: S55333; MUID:95300786; PMID:7781606
A;Accession: S55333
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A;Molecule type: mRNA
A;Residues: 'M',61-370 <VA3>
A;Cross-references: UNIPARC:UPI00000278BF; GB:L41495; NID:g765065;
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C;Comment: Pim-2 autophosphorylates
C;Genetics:
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A;Molecule type: mRNA
A;Residues: 'M',27-370 <VA2>
A;Cross-references: UNIPARC:UPI00000278BE;
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A; Residues: 1-370 < VAN>
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Pred. No. 5.4e
40; Mismatches
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                     GB/EMBL/DDBJ
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A; Map position: 3
A; Introns: 72/3; 160/3;
C; Superfamily
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A;Gene: CESP:C06E8.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, Februa A:Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C06E8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-199 #sequence_revision 20-Sep-1999 #text_change C;Accession: T15435
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A;Cross-references: UNI
A;Experimental source:
C;Genetics:
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TGEVKLVDFGATAYAEKATKKEFQGTRSYCPPEWFRDQLYLPLEATSWSLGVLLFILLTG
                           RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG
                                                        MERPANCMDLFDMVSVHGPLNEDMGKF1FKQV1TTVFNMYSKHGLLHRD1KDENL1VNMN
                                                                                                                 GOOPVAVKEVOHKHVRSW-TMTCROLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV
                                                                                                                                          -NLPVAIKHVEKDRISDWGELFNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLI
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ce: strain Bristol N2
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                                                                                                                                                                                                                                                                                                                                                                                                                             Z18350
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                                                                                                                                                                                                                             Score 495; DB 2; Length 40
Pred. No. 1.6e-17;
57; Mismatches 129; Indels
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9; Mismatches
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legans cosmid
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RESULT 8
S66730
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A;Title: Identification of novel protein kinases expressed A;Reference number: 149071; MUID:95200798; PMID:7893599
A;Accession: 149072
A;Cross-references:
A;Map position: 15L
C;Keywords: ATP
                                        A; Molecule type: DNA
A; Residues: 1-1101 <ANS>
A; Cross-references: UNIPROT: Q08217;
A; Experimental source: strain $288C
C; Genetics:
                                                                                                                                                                                     hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision
C;Accession: I49072
R;Ruiz, J.C.; Conlon, F.L.; Robertson,
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R;Ansorge, W.; Benes, V.;
submitted to the Protein
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A; Residues: 1-481 < RES>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPV
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                                                                                                                                                                                                                                                                                                         NLPTLRQRVLEGRERIPFEMSQDCETLIRRMLVVDPAKRITIAQIRQHRWMQ
                                                                                                                                                                                                                                                                                                                                  ----EEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQ
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                              SGD: S0005405
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33.2%;
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                                                                                                                                                           s.;
                                                                        UNIPARC: UPI000012DF35;
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                                                                                                                                                           Schwager,
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July 1996
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hypothetical protein 2255.8 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change O;Accession: T13741
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A;Introns: 205/3; 227/1; 322/3; 688/3;
A;Note: EG:22E5.8
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A; Residues: 1-1398 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: Sequencing the distal X chromosome o A;Reference number: 217668 A;Accession: T11741 A;Status: preliminary; translated from GB/EMBL/DDBJA;Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Murphy, L.; Harris, D.; Barrell, B. submitted to the EMBL Data Library, April 1999 A;Description: Sequencing the distal X chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:077268; UNIPARC:UPI00000820A3; EMBL:AL031765; NID:e1371523;
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Best Local Similarity
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Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                          VYSPPEWIRYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIVKGQVYFRQRV
                                                                                                                                                                                              KFWQIISAVEYCHKKGIVHRDLKAENLLLDLNM-NIKIADFGFSNHFKPGELLATWCGSP
                                                                                                                                                                                                                                                                                              YREVEIMKRLK--HPHIIKLYQVMETKNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF
                                                                                                                                                                                                                                                                                                                                                PMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARS 146
                                                                                                                                                                                                                                                                                                                                                                                                  KLKEPMRVGFYDIERTIGKGNFAVVKLARHRITKN-EVAIKIIDKSQL----DQTNLQKV
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SSECEHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL
                                         SSECOHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLL
                                                                                             PYAAPEVFEGKQYTGPEIDIWSLGVVLYVLVCGALPFDGSTLQSLRDRVLSGRFRIPFFM
                                                                                                                                                                                                                                             FFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFG-SGALLKDTVYTDFDGTR 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 374; DB 2;
Pred. No. 3.2e-11;
57; Mismatches 110
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Pred. No. 2.6e-11;
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probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence revision 02-Aug-1994 #text_change 05-Oct-2004
C;Accession: S33653; S36717; S36732; JH0486
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
Yeast 9, 543-549, 1993
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
A;Reference number: S33653; MUID:93311122; PMID:8322517
A;Accession: S33653
A;Status: nucleic acid sequence not shown
A;Residues: 1-1358 <CLA>
A;Cross-references: UNIPROT:P31374; UNIPARC:UDF1000017A449; EMBL:L05146
A;Cross-references: UNIPROT:P31374; UNIPARC:UDF1000017A449; EMBL:L05146
A;Cross-references: UNIPROT:P31374; UNIPARC:UDF1000017A449; EMBL:L05146
A;Residues: 1-1358 <CLA>
A;Residues: 1-1358 <CLA>
A;Residues: 1-1359 <CLA>
A;Residues: 1-
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S33653
A;Molecule type: DNA
A;Residues: 1-864,867-1358 <OUE>
A;Residues: 1-864,867-1358 <OUE>
A;Cross references: UNIPARC:UPI0000052EA6; EMBL:L05146; NID:gl71851; PIDN:AAC04940.1;
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey,
Yeast 8, 133-145, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: catalyzes the formation of peptidy1-serine-phosphate or C;Superfamily: SNF1-related protein kinase; protein kinase homology C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein F;6-260/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P93113; A;Experimental source: cv. Masterpie C;Function:
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Pred. No. 3e-11;
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A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI000012DE43; R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P. submitted to the EMBL Data Library, May 1995

A; Description: Differential

accumulation

of the

transcripts

õ

22

novel

protein

GB:M93023;

NID:g166599;

PIDN

A; Molecule | A; Residues:

A;Status: preliminary A;Molecule type: DNA A; Reference number: S58256 A; Accession: S58266 A;Reference number: JC1446; MUID:93013041; PA;Accession: JC1446

A; Molecule type: DNA A; Residues: 1-512 < LEG>

R;LeGuen, L.; Thomas, M.; Gene 120, 249-254, 1992

Bianchi,

M.; Halford,

#text_change

AK21 -

Arabidopsis

thaliana

e from Arabidopsis PMID:1339373 N.G.; Kreis,

thaliana

encoding

Ø

serine/threonine-specific protein kinase (EC 2.7.1.-)
N;Alternate names: protein kinase NF1 homology
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #tc
C;Accession: JC1446; S58266; S66334

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A;Molecule type: DNA
A;Residues: 1-72,'E',7
A;Cross-references: UN
C;Genetics:
A;Gene: SGD:FUN31; SSP
A;Cross-references: SG
A;Cross-references: SG
A;Map position: 1L
C;Keywords: ATP; glyco
F;1096-1356/Domain: pr
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R;Sidhu, R.S.; Mathewes, S.; Bollon, A.P.
Gene 107, 111-118, 1991
A;Title: Selection of secretory protein-encoding genes l
A;Reference number: JH0483; MUID:92077420; PMID:1743509
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F;1232/Active
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A;Status: translation not sho
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;1096-1356/Domain: protein kinase homology <KIN>;11094-1112/Region: protein kinase ATP-binding motif;8 128/Binding site: carbohydrate (Asn) (covalent) #;1232/Active site: Asp #status predicted
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                                                                                                                                                                        VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIR
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RCVPKRPTIDDINNDKWL
                                 LRPSDRPSFEEIQNHPWM
                                                                       GNPYEGOPODIWAIGILLYTVVFKENPFYNIDEILEGDLKFNNAEEVSEDCIELIKSILN
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UNIPARC:UPI000017A44B
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Pred. No. 7.7e-11;
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A;Accession: C.C., A;Accession: C.C., A;Accession: A;Accession: A;Accession: A;Accession: A;Residues: 1-798 <a href="https://www.ncs.upi0000044792">xXIA> A;Residues: 1-798 <a href="https://www.ncs.upi0000044792">xXIA> A;Cross-references: UNIPROT:Q9IA88; UNIPARC:UPI0000044792; GB:AF219232 A;Cross-references: UNIPROT:Q9IA88; UNIPARC:UPI00000044792; GB:AF219232 A;Cross-references: UNIPROT:Q9IA88; UNIPARC:UPI000000044792; GB:AF219232 A;Cross-references: UNIPROT:Q9IA88; UNIPARC:UPI00000044792; GB:AF219232 A;Cross-references: UNIPROT:Q9IA88; UNIPARC:UPI00000044792; UNIPARC:UPI00000044792; UNIPARC:UPI00000044792; UNIPARC:UPI00000044792; UNIPARC:UPI00000044792; UNIPARC:UPI00000044792; UNIPARC:UPI00000044792; UNIPARC:UPI0000044792; UNIPARC:UPI0000044792; UNIPARC:UPI00000044792; UNIPARC:UPI0000044792; UNIPARC:UPI0000044792; UNIPARC:UPI000044792; UNIPARC:UPI000044792; UNIPARC:UPI000044792; UNIPARC:
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A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C;Function:
A;Description: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonir C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,44/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
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Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
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N;Alternate names: Qin-induced kinase
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A;Residues: 144-198 <"H2>
A;Cross-references: UNIPARC:UPI000009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1;
C;Comment: This enzyme plays an important role in a signal transduction cascade regula
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    YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS
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                                                                                                                     Score 357.5; DB 2; Pred. No. 1.3e-10;
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RESULT S52244

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p69Eg3 protein

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R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A;Title: Regulatory interaction of PRLI WD protein with Arabidopsis SNF1-like A;Reference number: Z25116; MUID:99238528; PMID:10220464
A;Accession: T52633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - N;Alternate names; SNF1 protein kinase omolog AKIN11 C;Species: Arabidopsis thaliana (mouse-car cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 05-Oct-2004 C;Accession: T52633
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A; Residues: 1-512 <BHA>
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                                     QHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
                                                                            EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSEA
                                                                                                                  EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----VKGQVY-FRQRVSSEC
                                                                                                                                                                                                                                      ILRLFM--HPHIIRQYEVIETTSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQI
                                                                                                                                                                                                                                                                                                                     ESILPNYKLGKTLGIGSFGKVKIAEHVVTGHKVAIKILNRRKIKN---MEMEEKVRREIK
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: $52244
R;Roghi, C:; le Guellec, R:; Paris, J:; Couturier, A:; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Description: Eg3; selected by differential screening encodes a new Xenopus protein kin A;Reference number: $52243
A;Reference number: $52243
A;Recession: $52244
A;Stacus: preliminary
A;Molecule type: mRNA
A;Residues: 1-651 <ROG-
A;Cross-references: UNIPROT:091821; UNIPARC:UPI000017A463; EMBL:Z17205; NID:g609283; PID C;Keywords: ATP-
C;Keywords: ATP
F;11-265/Domain: protein kinase homology <KIN>
F;11-27/Region: protein kinase homology <KIN>
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ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
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                                                                                                                         MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0; Zakut-Houri R., Hazum S., Givol D., Telerman A.; Telerman A.; "The cDNA sequence and gene analysis of the human pim oncogene."; Gene 54:105-111(1987).
                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.

MEDLINE=90382681; PubMed=2205533; D

Reeves R., Spies G.A., Kiefer M., E

"Primary structure of the putative

Gene 90:303-307(1990).
                                                                                                                                                                                                                                                                 HOMO.
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Domen J., von Lindern
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIHLHSLSPSPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
                    Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLLSKINSLAHLRTAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFEHDEETIRGOVFFRORVSSECOHLIRWCLALRPSDRPSFEETONHPWMODVLLPQETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERPEPVODLEDFITERGALQEELARSFFWOVLEAVRHCHNCGVLHRDIKDENILIDLNRG
                                                                     . SEQUENCE.
3217305; PubMed=3329709;
                                                                                                                                                                                                                                                                                    ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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313
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                    1:103-112(1987)
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ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
ATP (COBE268D638E6967 CR
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Pred. No. 5.3e
4; Mismatches
                                                                                                                                                                                                       DOI=10.1016/0378-1119(90)90195-W;
Barr P.J., Power M.;
e human oncogene, pim-1.";
                                                                           Α.,
                                          PIM-1 cDNAs: nucleotide sequence f the in vitro synthesized PIM-1
                                                                             Breuer
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collaboration -

removed as This Swiss-Prot entry is copyright. It is produced the between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no

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RX MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., WcBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmtz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmtz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasqualucci L., Neumeister P., Goossens T., Nanjangud G., Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
"Hypermutation of multiple proto-oncogenes in B-cell diff cell lymphomas.";
Nature 412:341-346(2001).
                                                                                                                                                                                                              "Pim-1 protein kinase is nuclear in Burkitt's lymp localization is necessary for its biologic effects Anticancer Res. 23:167-178(2003).

-i- FUNCTION: Thought to play a role in signal tracells. May affect the structure or silencing ophosphorylating HP1 gamma/CBX3.

-i- CAPALYTIC ACTIVITY: ATP + a protein = ADP + a -i- SUBUNIT: Binds to RP9 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20130009; PubMed=10664448; DOI=
Koike N., Maita H., Taira T., Ariga H.,
"Identification of heterochromatin prot
phosphorylation target by Pim-1 kinase
phosphorylation on the transcriptional
FEBS Lett. 467:17-21(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22567470; PubMed=12680209; Ionov Y., Le X., Tunquist B.J., SweJohnson T., Lilly M.B., Kraft A.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Telerman A., Amson R., Zakut-Houri R., Givol D., "Identification of the human pim-1 gene product cytoplasmic protein with tyrosine kinase activit; Mol. Cell. Biol. 8:1498-1503(1988).
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Meeker T.C., Nagarajan L., Ar-Rus
subfamily.
DATABASE: NAME=Atlas Genet.
WWW="http://www.infobiogen.
                                                                                             TISSUE SPECIFICITY: Expressed primarily hematopoietic and germ line lineages. PTM: Autophosphorylated on tyrosine resisting Indianality: Belongs to the Ser/Thr protest.
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and characterization of the human
related to the protein kinases.";
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354098; PubMed=11460166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=2837645;
         . Cytogenet. Oncol. Haematol.;
.fr/services/chromcancer/Genes/PIM1ID261.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sweetenham J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOI=10.1016/S0014-5793(00)01105-4;
a H., Iguchi-Ariga S.M.M.;
protein 1 (HPI) as a
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AMBL; M2750: AAA5000.

EMBL; M16750; AAA50471; -,
EMBL; M24915; AAA364471; -,
EMBL; M54915; AAA364471; -;
EMBL; M54915; AAA36153.1; -;
EMBL; M54979; AAA81553.1; -;
EMBL; BC020224; AAA70871.1; -;
EMBL; BC020224; AAA70871.1; -;
EMBL; AAA77871.1; -;
EMBL; AAA787871.1; -;
EMBL; AAA787871.1; -;
EMBL; AAA788779; TYHUP1.

AR PDB; 1XQ2; X-ray; A=14-313.

AR PDB; 1XR1; X-ray; A=14-313.

DR PDB; 1XW3; X-ray; A=13-305.

DR PDB; 1Y14; X-ray; A=33-305.

DR PDB; 1Y14; X-ray; B=1-313.

DR PDB; 1Y14; X-ray; B=1-313.

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DOMAIN
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313 AA; 35686
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MIM; 1649
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GO; GO:00
GO; GO:00
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PROSITE; PS00107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0004674; F:protein serine/threonine kinase activity
GO; GO:0007275; P:development; TAS.
GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR0008271; Ser_thr_pkin_AS.
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EIHLHSLSPSPSK
                                     PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
                                                                                                                                              ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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                                                                                                ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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107; PROTEIN KINASE ATP; 1.
011; PROTEIN KINASE DOM; 1.
108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nuclear
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Pred. No. 7.4e
6; Mismatches
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ATP (By similarity).
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7.4e-113;
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R Ensembl; ENSG00000137193; Homo sapiens.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004574; F:protein serine/threonine kinase activity
R GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.
R GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
R GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
R GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
R Interpro; IPR000719; Prot kinase.
R Interpro; IPR002290; Prot kinase.
R Interpro; IPR002290; Ser_thr_pkinase.
R Interpro; IPR001245; Tyr_pkinase.
R Interpro; IPR001245; Tyr_pkinase.
R Interpro; IPR001245; Tyr_pkinase.
R Ffam; PF00069; Pkinase; 1.
R SMART; SM00219; TyrKc; 1.
R SMART; SM00219; TyrKc; 1.
R R SMART; SM00219; TyrKc; 1.
R PROSITE; PS00107; PROTEIN KINASE DOM; 1.
R PROSITE; PS00107; PROTEIN KINASE DOM; 1.
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
R PROSITE; PS00108; PROTEIN KINASE TYROSITE; PS00108; PROTEIN KINASE; PROTEIN KINASE; TYROSITE; PS00108; P
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01-FEB-2005 (TrEMBLrel. 29, Last sequence up
01-FEB-2005 (TrEMBLrel. 29, Last annotation
Pim-1 oncogene (Proviral integration site 1)
Name=PIM1; Offinames=RP3-355M6.1-003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; E
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17 HUMAN
17 HUMAN PRELIMINARY;
05T7H7;
05T7H7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitted (WAY-2005) to the EMBL/GenBank/DDBJ databases. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosph SIMILARITY: Belongs to the Ser/Thr protein kinase fa L; AL535379; CAI20316.1; -; Genomic_DNA.
301
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                          EIHLHSLSPSPSK 313
                                                                             ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                                                                                                            ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
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                                                                                                                                                                                                                                                      ERPEPVQDLFDF1TERGALQEELARSFFWQVLEAVRHCHNCGVLHRD1KDEN1L1DLNRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.1%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1636; DB:
Pred. No. 7.4e-1
6; Mismatches
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nes 3;
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activity; IEA.
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IMI BOVIN

PIM1 BOVIN

D PIM1 BOVIN

STANDARD;

C Q9N0F9;

OT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2005 (Rel. 48, Last annotation update)

T 13-SEP-2005 (Rel. 48, Last annotation update)

T 13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Sim:
Matches 304;
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NP_BIND
ACT_SITE
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MEDLINE-21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;

Mang Z., Petersen K., Meaver M.S., Magnuson N.S.;

"CDNA cloning, sequencing and characterization of bovine pim-1.";

Vet. Immunol. Immunopathol. 78:177-195(2001).

-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-1- SUBUNIT: Binds to RP9 (By similarity).

-1- SUBCELULAR LOCATION: Cytoplasmic and nuclear (By similarity).

-1- SUBCELULAR LOCATION: Cytoplasmic and nuclear (By similarity).

-1- SUBCELULAR LOCATION: Cytoplasmic and nuclear (By similarity).
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nuclear protein; Nucleotide-binding; Phosphorylation; Proto-oncogene; Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Prot kinase.
InterPro; IPR0008271; Ser Thr pkin_AS.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF259078; AAF67200.1;
HSSP; Q63450; 1A06.
SMR; Q9N0P9; 32-308.
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                                                                                     ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                                         ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG
PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
                                                                                                                                                             ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENILIDLNRG
                                                                                                                                                                                                                                                                    NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL
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167
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nilarity 97.1%;
Conservative
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52 A.
167 P.
67 A.
35630 MW;
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Pred. No. 2.1e-11
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proton acceptor (By ATP (By similarity); 9EF40229A847AD47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein kinase.
ATP (By similarity).
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; Ruminantia;
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RX MEDLINE-22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Lableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
STRAIN=C57BL/6; TISSUE=Brain; Strausberg R.; Submitted (JUN-2003) to the E
                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
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Mammalia; Eutheria; Eu
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel.
10-MAY-2005 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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c. Natl. Acad. Sci. U.S.A.
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Euarchontoglires;
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                                                                                                                                                                                                                                                                                 n = ADP + a phosphoprotein.
protein kinase family.
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                                                                kinase activity;
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Best Local S
Matches 296
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        INTERACTION WITH RP9.

MEDLINS=20389540; PubMed=10931201;

Maita H., Harada Y., Nagakubo D., Kitaura H., Iked

Maita H., Harada Y., Iguchi-Ariga S.M.M.;

"PAP-1, a novel target protein of phosphorylation

Eur. J. Biochem. 267:5168-5178 (2000).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a

-!- SUBUNIT: Binds to RP9.
                                                                                                                                                                                                                                                                              Selten G., Cuypers H.T., Boelens W., Robomen J., van Beveren C., Berns A.; "The primary structure of the putative homology with protein kinases."; Cell 46:603-611(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
Muroidea; Muridae; M
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13-SEP-2005
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MEDLINE=86272109; PubMed=3015420;
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Euarchontoglires; Glires; Rodentia;
Murinae; Mus.
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DOI=10.1016/0092-8674(86)90886-X; V., Robanus-Maandag E., Verbeek J.

Euteleostomi; ia; Sciurognathi;

oncogene

pim-1

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Ikeda

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Tamai

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kinase.";

(By similarity) phosphoprotein

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InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; pp00069; pkinase; 1.
ProDom; pD000001; prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; pS00108; pROTEIN_KINASE_DOM; 1.
PROSITE; pS00108; pROTEIN_KINASE_T; 1.
PROSITE; PS00108; pROTEIN_KINASE_T; 1.
PROSITE; PS00108; pROTEIN_KINASE_T; 1.
SPROSITE; PS00108; pROTEIN_KINASE_T; 1.
SPROSITE; PS00108; pROTEIN_KINASE_T; 1.
SPROSITE; PS00108; pROTEIN_KINASE_TCTANSFERSE.
SEQUENCE 313 AA; 35451 MW; 1294F16A03B7C7D7 CR
Name=Pim1; Synonyms=Pim-1;
                      Proto-oncogene serine/threonine-protein
                                                                                                                                                                                                                                                                                                                    ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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94.6%;
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Last annotation updat
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Pred. No. 2.2e
8; Mismatches
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                      update)
in kinase
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2.2e-109;
es 9;
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                      Pim-1
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                      2.7.1.37).
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RESULT 8

PIM3 COTVA

ID PIM3 COTVA

AC Q9PUB5;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2005 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)

GN Name=PIM3; Synonyms=PIM-3;

OS Coturnix coturnix japonica (Japanese quail).
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Best Local S
Matches 295
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R HSSP; Q63450; 1A06.

R SMR; P0663; 32-308.

R Ensembl; ENSMUSG0000024014; Mus musculus.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR000271; Ser Thr _pkin_AS.

R Pfam; PF00069; Pkinase; 1.

R ProDom; PD000001; Prot kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

R PROSITE; PS00108; PROTEIN KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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NP BIND
ACT SITE
BINDING
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PIR; A24169; TVMSP1.
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94.2%;
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ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
MW; 79F4779E9DCBDC16 CR
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Pred. No. 5
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es 10;
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Best Local S
Matches 212
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BINDING
SEQUENCE
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MEDLING=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;

Bichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;

"Developmental expression of Pim kinases suggests functions also outside of the hematopoietic system.";

Oncogene 19:1215-1224(2000).

-i- CAPALYTIC ACTIVITY; ATP + a protein = ADP + a phosphoprotein

-i- PTM: Autophosphorylated.

-i- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PII
                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000001; Prot_kinase; 1.

SMART; SM00120; S.TKC; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ130845; CAB62386.1; -; HSSP; Q63450; 1A06. InterPro; IPR000719; Prot_kinas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                           Serine/threonine-protein kinase; Transferase
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InterPro; IPR002290; Ser_
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212; Conserv
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                                                MLLSKINSLAHL-RAAPCNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIRV
                                                                                                                  RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG
                                                                                                                                                                    ADNLFVAIKHVEKDRISDWGELFNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERFDSFVL
                                                                                                    TGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWS
                                                                                                                                                       VMERPELVKDLFDFITEKGALDEDTARGFFRQVLEAVRHCYGCGVVHRDIKDENLLVDLR
                                                                                                                                                                                                        ADGLPVAVKHVVKERVTEWGTI-GGVMVPLEIVLLKKVGSGFRGVIKLLDWYERPDGFLI
                                                                                                                                                                                                                                                          MLLSKFGSLAHICSPASMDHLPVKILPPVKVEKEPFDKVYQVGSVLGSGGFGTVYAGSRT
EDCDIRLRTLDTDVS
                        ATAEIHLHSLSPSPS
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IPR008271; Ser_thr_pkin_AS.
IPR002290; Ser_thr_pkinase.
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ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
E2A4FA20B6F6396C CRC64;
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RESULT 9
PIM3_HUMAN
ID PIM3_HUMAN

STANDARD;

PRT;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Gouldin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McCEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Hitling M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human and more colous colous and malysis of more than 15,000 full-length human
                       HGNC; HGNC
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comput. Biol. Chem. 27:29-35(2003).
-!- FUNCTION: May be involved in cell cycle progression and apoptosis process. Implicated in proliferation of human cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22682943, PubMed=12798037; DOI=
Chichester C., Nikitin F., Ravarini J.
"Consistency checks for characterizing
Comput. Biol. Chem. 27:29-35(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatocellular carcinoma development of human hepatoma cell lines."; Int. J. Cancer 114:209-218(2005).
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Mammalia; Eutheria;
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29-MAR-2004 (Rel.
13-SEP-2005 (Rel.
                                                                                  Ensembl;
                                                                                                       EMBL; AB114795; BAD42438.1; EMBL; BC052239; -; NOT_ANNO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Aberrant expression of serine/threonine hepatocellular carcinoma development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujii
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                                                                                                                                                                                                                                                                                                                                 Cell lines.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprot CATALYTIC ACTIVITY: Widely expressed. No expression in cc TISSUE SPECIFICITY: Widely expressed in human hepatoma thymus, and small intestine. Expressed in human hepatoma lines but not in normal liver tissues.

SIMILARITY: Belongs to the Ser/Thr protein kinase family
                                                                                                                                                                                                                               s Swiss-Prot entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
  HGNC:19310; PIM3
Pro; IPR000719; P
Pro; IPR008271; S
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ENSG00000198355;
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Mukaida N.;
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i J.-C., Lisacek F.;
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STRAIN-FVB/N, TISSUE-Colon, and Salivary gland;

RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Foshiyuki S., Carrinci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Foshiyuki S., Carrinci P., Prange C.,

RA BAS S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McDewan P.J., McKernan K.J., Malek J.A., Gy L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 220
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NP BIND
ACT SITE
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae: Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003
13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIM3
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Probom; PD000001; Prot_kinase; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00110; PROTEIN_KINASE_STM; 1.

PROSITE; PS00108; PROTEIN_KINASE_STM; 1.

PROSITE; PS00108; PROTEIN_KINASE_STM; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Pim3;
                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAPE-SCDLRLCTLDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM--QDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLLVLERPEPAQDLFDFI
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46
170
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326 AA;
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(Rel. 41,
(Rel. 48,
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69.6%;
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Last annotation
ein kinase Pim-3
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ATP (By similarity).
Proton acceptor (By and ATP (By similarity).
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Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; oglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41FDF9DD2467A162
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                                                                                                                                                                                                                                                                                                                                                                                                                MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
(EC 2.7.1.37).
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RESULT 11
PIM3_RAT
      BBDTTAC
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Best Local :
PIM3_RAT STANDARD; PRT; 326 AA.
070444;
08-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)
Kid-1) (Kinase induced by depolarization).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN

NP BIND

ACT SITE

BINDING

SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length hand mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-I- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom, PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
Serin/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI; MGI:1355297; Pim3.
InterPro; IPR0002719; Prot kinase.
InterPro; IPR008271; Ser thr pkin
InterPro; IPR002290; Ser thr pkina
Pfam; PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC017621; AAH17621.1;
EMBL; BC026639; AAH26639.1;
HSSP; Q03656; 1HOW.
Ensembl; ENSMUSG000000035828
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                                                                                                                                                                                                                                        VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM
                                                                                                                                                                                                                                                                                                                       DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM
                                                                                                                                                                                                                                                                                                                                                                         FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV
                                                                                                                                                                                                                                                                                                                                                                                               FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI
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                                                                                                                                                                                                                    VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM
                                                                                                                                                                                                                                                                                              DLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM
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46
170
69
326 AA;
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54 A;
170 P;
69 A;
35970 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein kinase.

ATP (By similarity).

Proton acceptor (By similarity).

ATP (By similarity).

M; DD68CBF46354851E CRC64;
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                        (Protein
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                          kinase
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Best Local S
Matches 214
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MEDLINE-98298176; PubMed-9639723; DOI=10.1074/jbc.273.26.16535;
REDLINE-98298176; PubMed-9632723; DOI=10.1074/jbc.273.26.16535;
Peldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
Bazan N.G., Baudry M., Herschman H.R.;
Bazan N.G., Baudry M., Herschman H.R.;
"KID-1, a protein kinase induced by depolarization in brain.";
"KID-1, a protein kinase induced by depolarization in brain.";
J. Biol. Chem. 273:16535-16543 (1998).

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-i- TISSUE SPECIFICITY: Present in a number of unstimulated tissu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat);
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                               ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclectide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF086624; AAC68900.1;
EMBL; AF057026; AAC36065.1;
HSSP; Q03656; 1HOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley;
KOnietzko U., Kuhl D.;
"Pim-3 is a member of the pim kinase family.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0004674; F:protein serine/threonine kinase GO; GO:00046777; P:autophosphorylation; IDA. GO; GO:0016572; P:histone phosphorylation; IDA. InterPro; IPR000719; Prot kinase.

InterPro; IPR002290; Ser_thr_pkin_AS.

InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF057026; AA
HSSP; Q03656; 1HOW
RGD; 620462; Pim3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               removed
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INDUCTION: By membrane depolarization
PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Swiss-Prot entry is copyright. It is produced through a cent the Swiss Institute of Bioinformatics and the EMBL Eduropean Bioinformatics Institute. There are no restrict as long as its content is in no way modified and this state
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                                                                                                                                                                                  Similarity
                                                   MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKYYQVGAVLGSGGFGTVVAGSR
                                                                                                                                         MILSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV
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                                                                                                                                                                                                                                         Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
                                                                                                                                                                      Score 1131.5; DB
Pred. No. 1.6e-75;
D; Mismatches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity;
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F. Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Ahtiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Scheutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schentz J., Myers R.M.,
RA RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA ROdriguez A.C., Grimwood J., Schentz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
    Query Match
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Matches 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2005) to the EMBL/GenBan
-! SIMILARITY: Belongs to the Ser/Thr
EMBL; BC097317; AAH97317.1; -; mRNA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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"ATEMBLICAL 31, Last sequence update)
"ATEMBLICAL 31, Last annotation update
Hypothetical protein (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chillian Met
                                                                                                                                                                                                                  ProDom; P000001; Prot kinase; 1.
SMART; SM00220; S_TKC; 1.
SWART; SM00220; S_TKC; 1.
SWART; SM002219; TyrKC; 1.
PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Hypothetical_protein; Kinase; Nuc
Serine/threonine-protein kinase; Transferase.
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Mammalia; Eutheria; Euarchontoglires; Glires;
Muroidea; Muridae; Murinae; Rattus.
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                                        Similarity
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l. Acad. Sci. U.S.A.
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the Ser/Thr protein
-; mRNA.
                                        Score 1131.5;
Pred. No. 1.9
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lires; Rodentia; Sciurogna
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R HSSF; COLLING; 36-292.

R SMR; Q811X8; 36-292.

JR MGI; MGI:1355297; Pim3.

DR GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein maino acid phosphorylation;

DR GO; GO:0006468; P:protein maino acid phosphorylation;

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR008271; Ser thr_pkin_AS.

DR Pfam; PF000669; Pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Nucleotide-binding;

Serine/threonine-protein kinase; Transferase.

Serine/threonine-protein kinase; Transferase.
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Best Local S
Matches 213
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X8 MOUSE
Q811X8 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: Belongs to the EMBL/GenBank/DDBJ databases. EMBL; AY226239; AAK16606.1; -; mRNA. HSSP; Q03656; 1Q99. SMR; Q811X8; 36-292. SMR; Q811X8; 36-292.
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01-JUN-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mus musculus (mouse),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Pim3; Synonyms=Kid1;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q811X8,
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213; Conserv
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MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR
                                                                             VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS
                                                                                                                        MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR
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                                                                                                                                                                                    Conservative
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72.2%;
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Last seq
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Pred. No. 1.3e
1; Mismatches
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                                                             eonine kinase act phosphorylation;
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                                                                                                                                                                                                  1.3e-74;
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                                                                                                                                                                                                                                                 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                     ion; IEA.
                                                                                                                                                                                     Indels
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                                                             /IRLLDWFERPDG
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                                                                                                                                                                                    Gaps
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bhakesley R.W., Touchman J.W., Green E.D., Dickeon M.C.,
RA Bolakesley R.W., Touchman J.W., Green E.D., Dickeon M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                     GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity;
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000271; Ser_Ehr_pkin_AS.
InterPro; IPR000229; Ser_thr_bkinase.
InterPro; IPR001246; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Gerhard D.S.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-i- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; BC081340; AAH81340.1; -; mRNA.

SMR; O66111; 32-297.

Ensembl; ENSKETG0000009354; Kenopus tropicalis.
                                                                                           ProDom; PD000001; Prot_kinase;
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q66II1_XENTR
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                 Pfam; PF00069; Pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
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PS00107; PROTEIN_KINASE_ATP; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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28,
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EMBL; L29495; AAA85389.1; -; mRNA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PP00069; Pkinase; 1.
PROSITE; PS00107; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIM3 XENLA STANDARD; PRT; 323 AA (9)1822; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Serine/threonine-protein kinase Pim-3 (EC 2
                                                                                                                                                                                                                                                                                                                         Pim-1 proto-oncogene-encoded protein kinase.",
J. Biol. Chem. 272:10514-10521(1997).
-i- CATALYTIC ACTIVITY: ATP + a protein = ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 318 AA; 36547 MW; 48CCF12797F01FDC CRC64;
                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.

MEDLINE=97256736; Pubmed=9099695; DOI=10.1074/jbc.272.16.10514;

PALALY C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,

PALACY DE BOLOGE G. Tai G., Oh S., Amankawa L., Affolter M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Ver
Amphibia, Batrachia, Anura, Mesobatrachia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=PIM3; Synonyms=PIM1;
                                                                                                                                                           removed
                                                                                                                                                                           use as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kenopodinae; Kenopus; Kenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kenopus laevis (African clawed
                                                                                                                                                                                                                                           subfamily.

CAUTION: Was originally (Ref.1) called represent the pim-3 isoform.
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Treonine-protein kinase; Transferase. 40 291 Protein kinase. 40 291 Protein kinase. 46 54 ATP (By similarity). 46 54 ATP (By similarity). 46 65 ATP (By similarity). 47 Protein kinase. 48 Protein Acceptor (By similarity). 49 Protein acceptor (By similarity). 40 Protein Acceptor (By similarity). 41 Protein Acceptor (By similarity). 42 Protein Acceptor (By sutocatalysis). 43 Protein Acceptor (By sutocatalysis). 44 Protein Acceptor (By sutocatalysis). 45 Protein Acceptor (By sutocatalysis). 46 Protein Acceptor (By sutocatalysis). 46 Protein Acceptor (By sutocatalysis). 47 Protein Acceptor (By sutocatalysis). 48 Protein Acceptor (By sutocatalysis). 49 Protein Acceptor (By sutocatalysis). 40 Protein Acceptor (By sutocatalysis). 41 Protein Acceptor (By sutocatalysis). 42 Protein Acceptor (By sutocatalysis). 43 Protein Acceptor (By sutocatalysis). 43 Protein Acceptor (By sutocatalysis). 42 Protein Acceptor (By sutocatalysis). 43 Protein Acceptor (By sutocatalysis). 43 Protein Acceptor (By sutocatalysis). 42 Protein Acceptor (By sutocatalysis). 43 Protein Acceptor (By sutocatalysis). 43 Protein Acceptor (By sutocatalysis). 44 Protein Acceptor (By sutocatalysis). 45 Protein Acceptor (By sutocatalysis). 46 Protein Acceptor (By sutocatalysis). 46 Protein Acceptor (By sutocatalysis). 47 Protein Acceptor (By sutocatalysis). 48 Protein Acceptor (By sutocatalysis). 49 Protein Acceptor (By sutocatalysis). 40 Protein Acceptor (By sutocatalysis). 42
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US-08-463-074B-26
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Sequence 7, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HK
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 03500/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-09-237-543-7
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Similarity 100.0%; Pred. No. 9e-162;
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RESULT 2 US-09-644-450-7

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APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 313
TYPE: PAT
ORGANISM: Mus musculus
US-09-644-450-7
                                                                                                                          Sequence 8, Application US/09237543A

Patent NO. 6143540

GENERAL INFORMATION:
APPLICANT: Kapeller, ROSANA

TITLE OF INVENTION: NOVEL MOLECULES OF THE HK

TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631

CURRENT APPLICATION NUMBER: US/09/237,543A

CURRENT FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOFTMARE: PatentIN Ver. 2.0

SEQ ID NO 8

LENGTH: 313

TYPE: PRT

ORGANISM: Rattus norvegicus

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APPLICANT: Kapeller, Rosana
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100.0%; Pred. No. 9e-162;
ative 0; Mismatches 0;
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Pred. No. 3.4e-153;
8; Mismatches 10;
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Sequence 9, Application US/09237543A Patent No. 6143540
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GENERAL INFORMATION:
APPLICANT: KAPELICA: ROBANA
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CCURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 313
TYPE: PRT
ORGANIAN: Rattus norvegicus
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US-09-644-450-8
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ilarity 94.2%;
Conservative
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Pred. No. 3.4e-153;
8; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 313;
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LENGTH: 313;
TYPE: PRT;
ORGANISM: Homo sapiens
US-09-644-450-9
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US-09-644-450-9
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANY: Kapeller, Rosana
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                          Matches
                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL MOLECULES OF TITLE OF INVENTION: AND USES THEREOF PILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                        Local Similarity
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NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL
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                                                     MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD
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                                                                                                                      94.8%;
ilarity 93.9%;
Conservative 10
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93.9%; Pred. No. 5.4e-153;
tive 10; Mismatches 9;
                                                                                                                      10;
                                                                                                                    Score 1582; DB 2;
Pred. No. 5.4e-153;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                              THE HKID-1-RELATED PROTEIN FAMILY
                                                                                                                                                    Length 313;
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US-08-463-081B-26
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   Query Match
Best Local S
Matches 294
                                                                                                             TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
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                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/796,066
FILLING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: V1/11 A Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/104,736 FILING DATE: 10-AUG-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 444 South I
CITY: Los Angeles
STATE: California
COUNTRY: USA
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                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08463081B
     Conservative
                                                                                             peptide
94.7%; Score 1580; DB 1; 93.9%; Pred. No. 8.6e-153; tive 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/463,081E
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                                   Length 313;
   Indels
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TOPOLOGY: n.; MOLECULE TYPE: US-08-461-379A-26
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Query Match
Best Local Similarity
Matches 294; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-UNE-1995
PRIOR APPLICATION NUMBER: USN 08/330,108; 08/104,736
APPLICATION NUMBER: WORLD-1993,008/104,736
APPLICATION NUMBER: WORLD-1993,008/104,736
APPLICATION NUMBER: BOMBATAIN
APPLICATION NUMBER: 30,930
REPERENCE/DOCKET NUMBER: BORT-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5871961
GENERAL INFORMATION:
                                                                                                                                                                                                                                       TELEFAX: (610)470-0701 INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, TITLE OF INVENTION: Vector and Transformed Cell Thereof, and TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acid
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                                                                                                                                                       TYPE: peptide STRANDEDNESS: n.a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
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ADDRESSEE: (B) STREET:One Westlakes-Berwyn
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5. 5871961
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                                                                                                                                                                                              313 amino acids
            Conservative
                                                                                                                                      n.a.
                                                                                                              peptide
          94.7%; Score 1580; DB 1;
93.9%; Pred. No. 8.6e-153;
                                                 DB 1; Length 313;
          Indels
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            Gaps
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                                    ; MOLECULE TYPE: US-08-462-390B-26
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Query Match
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-CCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
                                                                                                                                                                   TELEFAX: (610)407-070
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                      FILING DATE: 20-NOV-91
ATTORNAY/AGENT INFORMATION:
NAME: Viviana Amzel, ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acid
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STATE: Pennsylvania
                                                                      TOPOLOGY:
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                                                                                           STRANDEDNESS:
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TD NO: 26:
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Length 313;
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US-08-463-074B-26
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US-08-463-074B-26
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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                                                                                                                  TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO:
                                                                                                                                               NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
            TOPOLOGY: n
MOLECULE TYPE:
                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
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                                                                                                SEQUENCE CHARACTERISTICS:
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                                           STRANDEDNESS:
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CITY: Los
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                                                                              313 amino acids
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0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadli
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Best Local Similarity 93.9
Matches 294; Conservative
                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION UNUBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Dh
                                                                    NAME: VIVIANA ANZEI, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
                                       TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 900071
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STATE: Californiaa
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                       LENGTH:
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                         313 amino acids
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. (B) STREET:
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and Expression There
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Suite

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Sequence 26, Application US
Patent No. 6057427
GENERAL INFORMATION:
APPLICANT: Smith, Kenda:
TITLE OF INVENTION: Nuc.
TITLE OF INVENTION: Pol.
TITLE OF INVENTION: Exp.
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
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US-08-652-446-26
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           FILING DATE: 5-JUN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/
                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: EP App. # 96921:
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION NUMBER: US/08/652,44
APPLICATION NUMBER: US/08/652,44
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                  RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
APPLICATION NUMBER: 08/463,074
                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
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Nucleic Acids Encoding CR5
Polypeptide, Vector and Transformed Cell Thereof, and
Expression Thereof
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93.9%; Pred. No. 8.6e-153;
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             08/462,337
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              CITY
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none
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US-07-857-224B-41
; Sequence 41, Application US/07857224B
; Patent No. 598784
; GENERAL INFORMATION:
; APPLICANT: Benner; Steven A.
; TITLE OF INVENTION: Predicting Folds
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-652-446-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/739,52
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/46
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/46
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213)
               ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/463,081
Zurich
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Pred. No. 8.6e-153;
0; Mismatches 9;
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60

300

240 240

300

COUNTRY:

Switzerland

code)

CH-8092

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; JOURNAL: Scier
; VOLUME: 241
; PAGES: 42-52
; PATE: 1988
US-07-857-2248-41
RESULT 14
US-09-237-543-5
; Sequence 5, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED |
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
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Best Local Similarity
Matches 256; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: Protein kinase; PUBLICATION INFORMATION: AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
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DESCRIPTION:
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LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase
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TOPOLOGY: linear
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                                                                                                                                                                                                PSDRPSFEEIRNHPWMQGD
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Pred. No. 5.2e.
0; Mismatches
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; LENGTH: 455
; TYPE: PRT
; ORGANISM: Rattus 1
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LENGTH: 455
TYPE: PRT
ORGANISM: Rattus r
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Best Local S
Matches 213
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Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
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Best Local Sim
Matches 213;
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
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CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
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                ILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL
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                                                                                                                            GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
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LLVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL
                                                      PDGFLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN
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31; Mismatches
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Post-processing: Minimum
Maximum
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Match
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Gapop 10.
        Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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1668
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  US-09-971-791-7
US-10-348-081-14
US-10-664-421-7
US-10-705-757-6
US-10-971-728-10
US-10-971-791-9
US-09-971-791-9
US-09-971-791-9
US-10-348-081-12
US-09-971-791-9
US-10-348-081-13
US-10-664-421-13
US-10-664-421-13
US-10-971-7268-9
US-10-951-407-18
US-10-951-407-18
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US-10-951-405-15-15-2
US-10-964-635-15-2
US-10-9620-052A-72
US-10-664-421-7
US-10-664-421-7
US-10-664-421-7
US-10-664-635-15-2
US-10-664-635-7
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US-09-971-791-7

Sequence 7, Application US/09971791

Patent No. US30020115120A1

GENERAL INFORMATION:
APPLICANT: Rosamna Kapeller-Libermann
APPLICANT: Laura A. Rudolph-Owen

APPLICANT: Kyle MacBeth

TITLE OF INVENTION: NOVEL MOLECULES OF THE HKI
FILE REFERENCE: 35800/238856

CURRENT APPLICATION NUMBER: US/09/971,791

CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/637,543
PRIOR FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTM: 13
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; TYPE: PRT
; ORGANISM: Mus musculus
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US-10-148-081-6
US-10-705-757-11
US-10-377-268-14
US-10-377-268-14
US-10-941-635-6
US-10-348-081-10
US-10-348-081-2
US-10-664-421-166
US-10-425-114-54275
US-09-971-791-5
US-09-971-791-6
US-10-425-114-54275
US-10-425-114-54275
US-10-377-268-16
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Pred. No. 8.1e-142;
; Mismatches 0;
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Title: Perfect score:

Run on:

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Scoring table: Sequence:

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Sequence 2. Application US/10664421

Publication No. US20040142864A1

Publicant INFORMATION:
APPLICANT: IBRAHIM, PRABHA
APPLICANT: IBRAHIM, PRABHA
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT PILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
IPRIOR FILING DATE: 2002-09-16
IPRIOR FILING DATE: 2002-09-16
IPRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
IPRIOR APPLICATION DATE: 2002-09-16
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SEQ ID NO 14
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity
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APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAVZ002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
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No. US20040038246A1
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100.0%; Pred. No. 8.1e-142;
htive 0; Mismatches 0;
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; LENGTH: 313;
; TYPE: PRT
; ORGANISM: Mus musculus
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Best Local Similarity 100.0%;
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Sequence 6, Application US/10705757
Publication No. US20040146942A1
GENERAL INFORMATION:
APPLICANT: GRUENENTHAL GMBH
TITLE OF INVENTION: SCREENING METHOD USING PIN
FILE REFERENCE: 029310.52818US
CURRENT APPLICATION NUMBER: US/10/705,757
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/EP02/05234
PRIOR APPLICATION NUMBER: DE 101 23 055.9
PRIOR APPLICATION NUMBER: DE 101 23 055.9
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: PRIOR 6
LENGTH: 313
TYPE: PRI
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                            y Match 100.0%; Score 1668; DB 4; Local Similarity 100.0%; Pred. No. 8.1e-142; hes 313; Conservative 0; Mismatches 0;
                                                                                                                                                                     1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
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Pred. No. 8.1e-142;
D; Mismatches 0;
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RESULT 6
US-10-941-635-2
; Sequence 2, Application US/10941635
; Publication No. US20050164300A1
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US-10-377-268-10
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PRIOR FILING DATE: 2003-01-02
PRIOR PELICATION NUMBER: 60/360,651
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 38
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Best Local Similarity 100.0%; 1
Matches 313; Conservative 0;
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APPLICANT: MILBURN, MICHAEL VANCE
TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
FILE REFERENCE: 039363/0303
CURRENT APPLICATION NUMBER: US/10/377,268
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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TYPE: PRT
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Pred. No. 8.1e-142;
0; Mismatches 0;
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LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus n
US-09-971-791-8
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; TYPE: PRT
; ORGANISM: Mus n
US-10-941-635-2
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US-09-971-791-8
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                                                                  GENERAL INFORMATION:

APPLICANT: Laura A. Rudolph-Owen
APPLICANT: Kyle MacBeth

ITILE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 35800/238856

CURRENT APPLICATION NUMBER: US/09/971,791

CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/634,450
PRIOR APPLICATION NUMBER: 09/637,543
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS 8

SEQ ID NO 8

SEQ ID NO 8
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APPLICANT: ARTIS, DE
APPLICANT: BREMER,
APPLICANT: GILLETTE
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PRIOR FILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09971791 Patent No. US20020115120A1
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Best Local !
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TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039363-1702
CURRENT APPLICATION NUMBER: US/10/941,635
CURRENT FILING DATE: 2004-09-15
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IBRAHIM, PRABHA L.
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GILLETTE, SAMUEL J.
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APPLICANT: WUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT APPLICATION APPLICATION OF THE 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOPTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 313
TYPE: NOT
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Best Local Similarity
Matches 295; Conserv
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Best Local
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                                                ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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94.2%;
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US-10-705-757-4
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Sequence 9, Application US/09971791

Patent No. US20020115120A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Vyle MacBeth
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 35800/238856

CURRENT APPLICATION NUMBER: US/09/971,791
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/237,543

PRIOR APPLICATION NUMBER: 09/237,543
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SEQ ID NO 4
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Best Local Similarity
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Pred. No. 3e-134;
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Matches 294;
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Matches 294
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CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20030045491A1
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
                                                                                                                                                                                                    LENGTH: 31
TYPE: PRT
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93.9%; Pred. No. 4.6e-134;
tive 10; Mismatches 9;
                                                                                                            10;
                                                                                                            Score 1582; DB 4;
Pred. No. 4.6e-134;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                              a Therapeutic
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PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 52
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Best Local Similarity
Matches 294; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SUNESIS PHARMACEUTICALS, INC.
APPLICANT: Prescott, John C.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394,322A
CURRENT FILING DATE: 2003-03-20
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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EIHLHSLSPGPSK 313
                          EIHLHSLSPGSSK 313
                                                                    PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
                                                                                                            ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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RESULT 13
US-10-348-081-13
; Sequence 13, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus

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APPLICANT: BREMER, RYAN
APPLICANT: IBRAHIM, PRABHA
APPLICANT: MILBURN, MICHAEL V.
APPLICANT: MALDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
APPLICANT: MILBURN, MICHAEL V.
APPLICANT: MILBURN, MICHAEL V.
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
NUMBER OF SEQ ID NOS: 169
SEQ ID NOS 1
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-664-421-1
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Query Match
Best Local Sim:
Matches 294;
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APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 13
LENGTH: 313
TYPE: TERMINATE OF THE TARGET FOR TYPE 2 DIABETES MELLITUS
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TYPE: TERMINATE SCHOOL TO THE TARGET FOR TYPE 2 DIABETES MELLITUS
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Best Local Similarity 93.9
Matches 294; Conservative
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                       94.8%;
93.9%;
; Score 1582; DB 4;
; Pred. No. 4.6e-134;
10; Mismatches 9;
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; Pred. No. 4.6e-134;
10; Mismatches 9;
                                                 DB 4; Length 313;
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US-10-664-421-150
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SEQ ID NO 150
LENGTH: 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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APPLICANT: IBRAHIM, PRI
APPLICANT: KUMAR, ABHII
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EIHLHSLSPGSSK 313
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EIHLHSLSPGPSK 313
                                                                                     PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
NUMBER OF SEQ ID NOS: 169
NUMBER OF SEQ ID NOS: 169
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KUMAR, ABHINAV
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; Score 1582; DB 4;
; Pred. No. 4.6e-134;
10; Mismatches 9;
                                                           Length 313;
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NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 180 240 240 180 120 120 60

Indels

<u>,,</u>

Gaps

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Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFBEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGSSK 313

Db 301 EIHLHSLSPGPSK 313

Search completed: May 4, 2006, 05:32:06

Job time: 93.6667 secs
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Result
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Perfect score:
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Maximum
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  1122.5
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2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep1:*

8: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep1:*

9: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep1:*

10: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep1:*

11: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep1:*

12: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep1:*
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Maximum Match 100%
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     GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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8 US-10-505-928-690

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9 US-11-877-346-72

11 US-11-113-424-183

11 US-11-087-099-11500

12 US-10-870-99-11726

12 US-11-087-099-11726

13 US-11-087-099-11726

14 US-11-087-099-11726

15 US-11-087-099-11726

16 US-11-087-099-11726

17 US-11-087-099-11726

18 US-11-087-099-11838

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18 US-11-087-099-12331

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US-10-511-937-2982

US-10-501-841-32

US-10-501-841-40

1 US-11-103-065-2
  US-10-501-841-37
US-10-784-004-435
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                                                Sequence 373, App
Sequence 2982, Ap
Sequence 32, Appl
Sequence 40, Appl
Sequence 90, Appl
Sequence 690, App
Sequence 77, Appl
Sequence 11500, Ap
Sequence 11500, Ap
Sequence 11726, A
Sequence 11726, A
Sequence 397, App
Sequence 397, App
Sequence 11838, A
Sequence 12331, A
Sequence 12331, A
Sequence 12331, A
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37, Appl
435, App
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324.5	324.5	324.5	325	325	325	325	325	325.5	326	326.5	328	328.5	329	329	333	334	334	336.5	338	341.5	342	342.5	344
19.5	19.5	19.5	19.5	19.5	19.5	19.5	19.5	19.5	19.5	19.6	19.7	19.7	19.7	19.7	20.0	20.0	20.0	20.2	20.3	20.5	20.5	20.5	20.6
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US-11-087-099-4237	US-11-087-099-8358	US-10-979-095-6	US-10-995-561-877	US-10-995-561-876	US-10-995-561-880	US-10-995-561-878	US-10-995-561-881	US-11-096-568A-32576	US-11-087-099-8865	US-10-204-639-17	US-10-204-639-65	US-11-087-099-905	US-11-096-568A-20430	US-11-096-568A-20431	US-11-087-099-3898	US-11-177-138-10	US-10-770-726-67	US-11-096-568A-18364	US-11-087-099-1886	US-11-087-099-12402	US-11-087-099-7631	US-11-096-568A-32575	US-10-784-004-951
Sequence 4237, Ap	æ		Sequence 877, App	Sequence 876, App	Sequence 880, App	Sequence 878, App	Sequence 881, App	Sequence 32576, A	e 8865,	Sequence 17, Appl	Sequence 65, Appl	Sequence 905, App	Sequence 20430, A	Sequence 20431, A	Sequence 3898, Ap	e 10	Sequence 67, Appl		Sequence 1886, Ap	Sequence 12402, A	Sequence 7631, Ap	e 3257	Sequence 951, App

ALIGNMENTS

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Sequence 373, Application US/10784004

Publication No. US20060084066A1

GENERAL INFORMATION:

APPLICANT: Biogen Idec
TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000

CURRENT APPLICATION NUMBER: US/10/784,004

CURRENT FILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 1251

SOFTWARE: PatentIn version 3.2

SEQ ID NO 373

LENGTH: 455
TYPE: PRT

ORGANISM: rat
US-10-784-004-373
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Best Local Similarity 71.0
Matches 213; Conservative
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YDMVCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWMLG
                                                                                                                       PDGFLLVLERPEPAQDLFDF I TERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDI KDEN
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RESULT

US-10-511-937-2982

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FILE FERRENCE: 506612000104

FILE REFERENCE: 506612000104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: DCT/US2003/012946

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTWARE: Patentin version 3.2

SEQ ID NO 2982

LENGTH: 334
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                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/10501841 Publication No. US20060084055A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Ordonez, Nadia
APPLICANT: Ordonez, Nadia
APPLICANT: Carteer, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection,
TITLE OF INVENTION: and Thorapy of Hematological Malignancies
FILE REFERENCE: 014058-014402PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
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Ly, Ngoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wohlgemuth, Jay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 334;
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APPLICANT: Mannion, Jane
APPLICANT: Wannion, Jane
APPLICANT: Wannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: Corixa Corporation
APPLICANT: McNeill, Particia Dianne
APPLICANT: McNeill, Particia Dianne
APPLICANT: McNeill, Particia Dianne
APPLICANT: Workerlion: Compositions and Methods for the Detection, Dia
TITLE OF INVENTION: and Therapy of Hematological Malignancies
FILE REFERENCE: 014058-014402PC
CCURRENT APPLICATION NUMBER: US/10/501,841
CCURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: WS 10/057,475
PRIOR APPLICATION NUMBER: WS 10/057,475
PRIOR APPLICATION NUMBER: WS 0FT/US03/02353
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR FILING DATE: 2003-01-22
NUMBER OF SEQ ID NO 40
LENGTH: 311
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CURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 10/057,475
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: WO PCT/US03/02353
PRIOR PILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 124
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 32
PENOTH: 334
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                                                                                               US-10-501-841-40
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathar
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Query Match 51.0%;
Best Local Similarity 60.5%;
Matches 161; Conservative 38
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Best Local Similarity 59.6%;
                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                              TYPE: PRT
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; Pred. No. 3.6e-67;
39; Mismatches 67;
Score 850; DB 9; Length 311; Pred. No. 8.2e-67; Mismatches 65; Indels
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RESULT 6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-103-065-2
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US-11-103-065-2
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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Publication No. US20050282189A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 161; Conserv
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CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,702
PRIOR APPLICATION NUMBER: 60/301,702
PRIOR FILING DATE: 2001-06-28
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TITLE OF INVENTION: 2150, Human Protein Kinase Family
TITLE OF INVENTION: Member and Uses Therefor
FILE REFERENCE: MPI2001-137PIRNM
                                                                                                          266 LIKWCLSLRPSDRPSFEEIRNHPWMQ 291
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                                                                                        LIRRCLAPKPSSRPSLEEILLDPWMQ 287
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 Application US/11087099
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; PUDILICATION:
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
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US-10-505-928-690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 9816
LENGTH: 504
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 690, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                        LENGTH: 661
TYPE: PRT
ORGANISM: Homo sapiens
105
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                                                                                                                                                             31 KEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEV 90
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                                                        EIMS--SLNHPHIISIYEVFENKDKIVIIMEYASK-GELYDYISERRRLSERETRHFFRO
                                                                           VLLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQ 150
                                                                                                                             KHNLKHRYELQETLGKGTYGKVKRATERFSGRVVAIKSIRKDKIKDEQDM----VHIRREI
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                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                    22.7%; Score 378.5; DB 8; 34.6%; Pred. No. 3.9e-25;
                                                                                                                                                                                                   47; Mismatches 114;
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                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: domain Consensus Sequence US-10-877-346-74
                                                                                                                                                                                                                    SOFTWARE: PatentIn
SEQ ID NO 74
LENGTH: 256
                                     Query Match
Best Local Similarity
Matches 97; Conserv
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PRIOR FILING DATE: 2001-09-26
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CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
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APPLICANT: MacDougall, John F
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                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/235,631 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-10-03
APPLICATION NUMBER: 60/238,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/236,065 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/235,633 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/237,434
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   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
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Padigaru, Muralidhara
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Smithson, Glennda
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Grosse, William M
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Lepley, Denise M
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                                       Conservative
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                                     22.4%; Score 373.5; DB 9; 36.6%; Pred. No. 3.2e-25; tive 45; Mismatches 100;
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                                       Indels
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RESULT 9
US-10-877-346-72
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CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT APPLICATION NUMBER: US/09/964,956
PRIOR APPLICATION NUMBER: US/09/964,956
PRIOR FILING DATE: 2001-09-26
PRIOR PELICATION NUMBER: 60/235,631
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR APPLICATION NUMBER: 60/235,838
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/236,064
PRIOR FILING DATE: 2000-09-27
PRIOR PELICATION NUMBER: 60/236,065
PRIOR PELICATION NUMBER: 60/236,065
PRIOR PELICATION NUMBER: 60/236,066
PRIOR PELICATION NUMBER: 60/236,066
PRIOR PELICATION NUMBER: 60/236,135
PRIOR APPLICATION NUMBER: 60/237,434
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,434
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
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                                                                                                 SOFTWARE: PatentIn Ver. SEQ ID NO 72
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                                                                                                                                                Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 127
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LENGTH: 256
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 YLHSRGIVHRDLKPENILLD-ENGTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       f: Shimkets, Richard A
INVENTION: Novel Proteins and Nucleic Acids Encoding
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Spytek, Kimberly A
Leach, Martin D
Shimkets, Richard A
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Smithson, Glennda
Millet, Isabelle
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Alsobrook II, John P
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Stone, David
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US-11-113-424-183
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                                                                      US-11-113-424-183
                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
PRIOR PPLICATION NUMBER: 60/311,613
PRIOR PPLICATION NUMBER: 60/315,617
PRIOR PPLICATION NUMBER: 60/315,617
PRIOR PPLICATION NUMBER: 60/307,506
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2001-05-02
   Query Match
Best Local S
Matches 92
                                                                                                                                                             NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 183
LENGTH: 256
Type: pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 183, A Publication No.
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PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic
                                                                                    FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R INFORMATION: 1
R INFORMATION: 2
R INFORMATION: 2
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   Similarity
92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQHLIKWCLSLRPSDRPSFEEIRNHPW 289
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o. US20050260713A1
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Serine/Threoniune protein kinase Co
Sequence
                                                                                                      Description
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                  22.3%;
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   52;
                  Score 371.5; DB 1
Pred. No. 4.8e-25;
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Pred.
                                                                                                     of Artificial Sequence:
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                                DB 11;
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 27;
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RESULT 12
US-10-501-035-357
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SEQ ID NO 11500
LENGTH: 514
TYPE: PRT
ORGANISM: Lycopersicon esculentum
US-11-087-099-11500
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US-11-087-099-11500
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                                                                                      Sequence 357, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local S
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINAS:
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REFERENCE: D0185 PCT
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TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
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                                                                                                                                                                                                                                                                                                                                                                        CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH
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                                                                                                                                                                                                                MLIVDPMKRMTIPEIRLHPWFQAHL
                                                                                                                                                                                                                                                                                                                  RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI----IKGQVF-FRQTVSSECQHLIKW
                                                                                                                                                                                                                                                                                                                                                    CHRNMVVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 191
                                                                                                                                                                                                                                                                                                                                                                                                                       HPH--IIRLYEVIETPSDIYVVMEYVKS-GELFDYİVEKGRLQEDEARNFFQQIISGVEY
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                                                                                                         Application US/10501035
o. US20060046249A1
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; Pred. No. 1.6e-24;
50; Mismatches 108;
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Sequence 11726, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 11726

CORGANISM: Hordeum vulgare

ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US 60/350,061
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE: PatentIn version 3.2
SEQ ID NO 357
LENGTH: 950
TYPE: PRT
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US-11-087-099-11726
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   Query Match
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ORGANISM: Homo sapiens
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   LNYAAPEIISSKLYAGPEVDVWSCGVVLYALLCGSVPFDDDNIPSLFRKIKGGTYILPSY 240
                                RVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDE-----EIIKGQVFFRQT-
                                                                                                 GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GT
                                                                                                                                     --EIKIMRLFIDFIHPHIIRVYEVIETPKDIFVVMEYCNN-GELLDYIIENGRLQEDEAR
                                                                                                                                                                    MEVVLLKKVSSDF--SGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLAR 145
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Sequence 3997, Application US/11087099
PUBLICATION NO. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Imperior of Section 1988 for Plant Imperior REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3997
LENGTH: 512
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US-11-087-099-3997
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US-11-241-056-11
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Best Local
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TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-US
CURRENT APPLICATION NUMBER: US/11/241,056
CURRENT FILING DATE: 2005-09-30
PRIOR APPLICATION NUMBER: US/09/980,464
PRIOR APPLICATION STATE: 2001-11-27
NUMBER OF SEQ ID NOS: 36
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TYPE: PRT
ORGANISM: Mus 1
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENILLD-ANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERPDSFYLILERPEPVODLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKVKKA-RESSGRLVAIKSIRKDKIKDEQDL---LHIRREIEIMS--SLNHPHIIAIHEV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDW 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALASESARP-----LADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTY
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Martin, Unja
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Search completed: May 4, 2006, 05:32:57 Job time: 16.3333 secs
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21.4%; Score 357; DB 11; Length 512;
Best Local Similarity 33.8%; Pred. No. 2.1e-23;
Matches 91; Conservative 53; Mismatches 101; Indels 24; Gaps 10;
                                                                                              188 ISGKLYAGDEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGYITLPSHLSAGARD 246
                                                                                                                                              247 LIPRMLIVDPMKRMTIPEIRLHPWFQAHL 275
                                                                      266 LIKWCLSLRPSDRPSFEEIRNHPWMOGDL 294
                                                                                                                    213 IRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----IK-GQVFFRQTVSSECQH 265
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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1: geneseqp1980;
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4: geneseqp2000;
5: geneseqp2002;
6: geneseqp2003;
7: geneseqp2003;
8: geneseqp2004;
9: geneseqp2004
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ALIGNMENTS

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AC A 26-JAN-1999; 99US-00237543. 23-AUG-2000; 2000US-00644450. 04-OCT-2001; 2001US-00971791. Mus musculus HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoietic neoplastic disor Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; WM; mouse. ABG33015 standard; protein; 313 22-AUG-2002. US2002115120-A1 Mouse protein 20-DEC-2002 ABG33015; (first entry) kinase phosphorylation site \$

Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.

WPI; 2002-712471/77.

Kapeller-Libermann R,

Rudolph-Owen LA,

Macbeth

(MILL-) MILLENNIUM PHARM INC.

Example 3; Page 38-39; 48pp; English.

The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method useful for modulating the level or activity of HKID-1 polypeptide or polynucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or

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The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with
                                    Claim 11;
                                                        Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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RESULT 3
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PN W020
YX 20-J
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The present sequence is the protein sequence of the murine serine/threonine protein kinase and proto-oncogene, PIM-1. E are the paralogues of novel human and murine PIM-3 proteins
                                                                       New human or murine PIM-3 DNAs or polypeptides, useful for agent for identifying anti-type 2 diabetes mellitus drugs, treating insulin resistance or type 2 diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS oneurodegenerative diseases). The present sequence is murine PIM1 kinase
                                                 Example 2;
                                                                                                                            WPI; 2003-598536/56
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                                                                                                                                                                                                                                                                          WO2003060130-A2
                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                  Mouse serine/threonine protein kinase
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 New transgenic mouse, useful as model system for the
                                                                                                                                                                                                                                                                                   Murine Piml
                                                                                                                                                                                                                                                                                                                                                               ADN97347 standard; protein;
                           WPI; 2004-099050/10.
                                                                                                                                 23-JUN-2003; 2003WO-US019818
                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                      mouse; probasin;
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                                                                                CALIFORNIA.
                                                    Ellwood-Yen
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                                                                                                                                                                                                                                                      promoter; transgenic mouse; c-myc; prostate cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a nucleic acid construct comprising a promoter having a fully defined nucleotide sequence comprising 310 bp (ADN97341), where the promoter is operably linked to c-myc having a fully defined nucleotide sequence comprising 1320 bp (ADN97342) where the c-myc protein encoded is expressed in prostate cells of the transgenic mouse at detectable levels. The transgenic mouse can be used as an in vivo model system for the study of prostate cancer and its progression. It can also be used in preclinical and clinical models to test novel diagnostic and therapeutic modalities including drug therapies relevant to prostate cancer prevention and progression. The transgenic animal can also be used to identify molecular markers that can be mediators of progression. Identification of the mediators is useful since they are potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapeutic targets. The present sequence represents murine Piml
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     EIHLHSLSPGSSK
                                      PFEHDEETIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEETRNHPWMQGDLLPQAAS
                                                            PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its progression comprising a nucleic acid construct comprising operably linked to c-myc gene encoded in prostate cells of mouse.
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Pred. No. 3.8e-158;
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RESULT 5
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XX
Mole
KW Mole
KW G-pr
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OS Mus
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DS Mus
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OS Mus
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OS Mus
XX
PD 02-S
XX
PD 02-S
XX
                                                                                                  G-protein coupled
                                                                                                                                                                                                      ADR88371 standard; protein;
           28-FEB-2003; 2003US-00377268
                                  02-SEP-2004.
                                                       US2004171062-A1
                                                                              Mus musculus
                                                                                                               Molecular
                                                                                                                                     Mus musculus
                                                                                                                                                          18-NOV-2004
                                                                                                               scaffold;
                                                                                                                                  PIM 1 protein.
                                                                                                                                                           (first
                                                                                                  d; nuclear hormone receptor; TNF receptor
receptor; methyl transferase; ligase; PII
                                                                                                                                                          entry)
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ligase;

PIM;

mouse

301

EIHLHSLSPGSSK 313

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RESULT 6
AEA19261
ID AEA1
XX AEA1
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XX MOUB
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Best Local S
Matches 313
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16-SEP-2002;
20-SEP-2002;
02-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method of designing a ligand binding to a target molecula. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the Mus musculus PIM 1 protein. This sequence is used to illustrate the method of invention.
                             artery
Pim-1.
                                                                   Mouse
                                                                                                                      AEA19261
                                                                                                                                              AEA19261 standard;
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nes 313; Conserv
  musculus
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                                         disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a ligand binding to a target molecule, comprises identifying scaffolds compounds binding to members of a molecular family, orientation of scaffolds at a binding site of target, and
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; 2002US-0411398P.
; 2002US-0412341P.
; 2003US-0437929P.
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                                         vasotropic; arteriosclerosis; antiarteriosclerotic;
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Pred. No. 3.8e-158;
Mismatches 0;
                                                                  sequence
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                                                                  SEQ
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RESULT 7
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Matches 313
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                                        micturition
PIM-1 prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                    Homo
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313; Conserv
                                                                      mouse
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                                       protein
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                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                        NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDPSGVIRLLDWFERPDSFVLIL
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                                        disorder;
in kinase;
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ilarity 100.0%;
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                                                                      serine-threonine
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                                                                                                                                   protein;
                                                                                          entry)
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                                        urinary dysfunction; uropathic; gene
serine-threonine kinase; enzyme.
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Pred. No. 3.8e-158;
Mismatches 0;
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                                                                       kinase
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DE102004004894-A1

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RESULT 8
AEA19263
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AC AEA1
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DT 28-C
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Best Local Similarity 100.0%;
Matches 313; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel method for identifying substances that regulate urinary incontinence and the urge to urinate. The method comprises incubating a test compound with a cell and/or cell preparation that has synthesized a specific protein of the PIM (proviral integration site) kinase family and measuring either binding of the test compound to the PIM kinase, or a functional parameter that is altered by the binding. The method of the invention demonstrates uropathic and gene therapy applications and may be useful for treatment and diagnosis of urinary incontinence and the urge to urinate. The method is based upon regulating the activity or expression of PIM kinases that are involved in bladder control. The current sequence is that of the house mouse PIM-1 serine-threonine kinase protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying substances that regulate PIM kinases, useful for treatment and diagnosis of urinary incontinence and the urge to urinate, and similar use of PIM proteins or nucleic acids.
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N-PSDB; AEB96040.
REFSEQ; NP_032868.
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            28-JUL-2005
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                                                      standard;
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                                                      protein;
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            entry)
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Pred. No. 3.8e-158;
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                                20-DEC-2002
          Rat protein
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standard;

protein;

kinase phosphorylation

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entry)

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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Therapeutic agent for comprises a component
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KATAKAMI N.
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               EIHLHSLSPGSSK
                                                                                                               EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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                                                        PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating artery disease e.g., arteriosclerosis, which inhibits the function of protein Pim-1.
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Pred. No. 1.5e-157;
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23-AUG-2000; 2000US-00644450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD
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                                                EIHLHSLSPGSSK 313
                                                                                                        PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA
                                                                                                                                     PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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Pred. No. 9
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Matches 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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N-PSDB; ABZ69187.
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                     EIHLHSLSPGSSK 313
                                                                                PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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 EIHLHSLSPSPSK
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94.2%;
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Pred. No. 9.9e-150;
B; Mismatches 10;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human or murine PIM-3 DNAs or polypeptides, useful for as a screening agent for identifying anti-type 2 diabetes mellitus drugs, or for treating insulin resistance or type 2 diabetes mellitus.
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                                                                                                                                                                                                                                                                                      Conservative
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Best Local (
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulate urinary incontinence and the urge to urinate. The method comprises incubating a test compound with a cell and/or cell preparation that has synthesized a specific protein of the PIM (proviral integration site) kinase family and measuring either binding of the test compound to the PIM kinase, or a functional parameter that is altered by the binding. The method of the invention demonstrates uropathic and gene therapy applications and may be useful for treatment and diagnosis of urinary incontinence and the urge to urinate. The method is based upon regulating the activity or expression of PIM kinases that are involved in bladder control. The current sequence is that of the Norway rat PIM-1 serine-threonine kinase protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying substances that regulate PIM kinases, useful for treatment and diagnosis of urinary incontinence and the urge to urinate, and similar use of PIM proteins or nucleic acids.
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N-PSDB; AEB96038.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFSEQ;
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94.2%;
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8; Mismatches
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                                                                                                                                                                       related to tyrosine threonine kinase (TTK, see ABP54938). TTK polynucleotides and polypeptides of the invention encompass polynucleotides and polypeptides having sequence similarity or sequence identity to human TTK and other genes and gene products related to TTK, such as Piml. The invention is based on the finding that TTK is differentially expressed in various forms of cancer. It provides methods for the identification of cancerous cells, especially breast cancer and colon cancer cells, by detection of expression levels of TTK, as well as diagnostic, prognostic and therapputic methods. These methods can be used as the basis of rational therapy. Assays for identifying molecules that modulate the activity of these genes in cancers, as well as methods of inhibiting tumour growth by inhibiting the activity of TTK are also
                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g growth of cancer cells comprises reducing Tyrosine Threonine
(TTK) activity, useful in diagnosing and treating disorders will expression levels and activity of TTK, such as lung, colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV73989
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                        The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method is activity of polypeptide, or level or activity of HKID-1 polypeptide or polynucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for
                                                                                                                                                                                                                                                                                                                                                          Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoletic neoplastic disor Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; WM; human.
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The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with
                                                                                                                  Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene pro
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.;
Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology
A;Reference number: A24169; MUID:86272109; PMID:3015420
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C;Genetics:
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A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
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EIHLHSLSPGSSK 313
                                                                                                                                           EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                                                                               EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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                                                PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
                                                                            PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
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Pred. No. 3.7e-74;
; Mismatches 0;
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A;Cross-references: UNIPROT: P26794; UNIPARC: UPI0000131AD6; EMBL:X63675; NID:g56902; PIDN A;Experimental source: testis
A;Note: testis-specific transcript is shorter and more stable than the somatic transcript C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Note: in testis may be involved in signal transduction events of normal germ cell matu C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F;44-52/Region: protein kinase ATP-binding mottif F;67/Active site: Lys #status predicted
                                                                                     protein kinase (EC 2.7.1.37) pim-1 - human N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene ()Species: Homo sapiens (man) C;Date: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004 C;Accession: JU0327; A46554; A27476; I58412 R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M. Gene 90, 303-307, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: $26298
A;Title: Primary structure of the putative human oncogene, A;Reference number: JU0327; MUID:90382681; PMID:2205533 A;Accession: JU0327 A;Molecule type: DNA
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A; Residues: 1-313 <WIN>
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94.2%;
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Pred. No. 4
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1.2e-70;
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RESULT S55333

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pim-2

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Gene 54, 105-111, 1987

A;Title: The cDNA sequence and gene analysis of the human pim oncogene.
A;Reference number: A27476; MUID:87277423; PMID:3475233
A;Accession: A27476
A;Molecule type: mRNA
A;Residues: 1-14, 'RA',17-313 <ZAK>
A;Cross-references: UNIPARC:UPI000014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:
A;Cross-references: UNIPARC:UPI000014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:
A;Cross-references: UNIPARC:UPI000014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:
A;Cross-references: UNIPARC:UPI000014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:
A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunolc
A;Reference number: 158412; MUID:88217305; PMID:3329709
A;Accession: 158412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-313 <DOM>
A;Cross-references: UNIPARC:UPI0000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PID:
C;Genetics:
C;Genetics:
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Almap position: 6p21.2-6p21.2

Allar position: 28/2; 63/3; 80/3; 203/1; 262/1

C; Function: 28/2; 63/3; 80/3; 203/1; 262/1

C; Function: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin G; Superfamily: kinase-related transforming protein; protein kinase homology C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F; 36-290; Domain: protein kinase homology cXIN>

F; 44-52/Region: protein kinase ATP-binding motif

F; 67/Active site: Lys #status predicted
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A;Title: Cloning and characterization of the human PIM-1 A;Reference number: A46554; MUID:88115604; PMID:3429489
A;Accession: A46554
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A;Residues: 1-313 <REB>
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI0000001060; GB:M27903; NID:g189958; R;Meeker T.C.; Nagazajan, L.; ar-Rushdi, A.; Croce, C.M.
J. Cell. Biochem. 35, 105-112, 1987
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A;Cross-references: GDB:119495; OMIM:164960
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A; Residues: 1-313 <MEE>
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                                                 EIHLHSLSPGSSK 313
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Pred. No. 5.2e-70;
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R;Percy, C. submitted to the EMBL Data committed to the EMBL Data committee to the EMBL Data
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A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;89-345/Domain: protein kinase homology <KIN>
F;89-105/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Mccession: A43093
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 'M',27-370 <VA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus muscui
C;Date: 10-Oct-1995 #
C;Accession: S55333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking A;Reference number: S55333; MUID:95300786; PMID:7781606
A;Status:
A;Molecul
                                A;Reference number:
A;Accession: T22255
                                                                                                        hypothetical protein F45H7.4 - Cal
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T22255
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A; Residues: 'M', 61-370 < VA3>
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A; Residues: 1-370 < VAN>
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                                                                                                                                                                                                                                                            EAELHFPAHVSPDCCALIRRCLAPKPCSRPSLEEILLDPWMQS---PAEEKPINSSKGSP
                                                                                                                                                                                                                                                                            GALLHDEPYTDFDGTRVYSPPEWISRHQYHALPATVWSLGVLLYDMVCGDIPFERDQEIL
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                   translated
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                                                                       Library,
                                                                                                                                                                Caenorhabditis elegans
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Pred. No. 3.4e-35;
1; Mismatches 87;
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                 GB/EMBL/DDBJ
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A;Residues: 1-363 <WIL>A;Cross-references: UNIDR
A;Experimental source: cl
C;Genetics:
A;Gene: CESP:F45H7.4
A;Introns: 72/3; 160/3; 3
A;Introns: 72/3; protein ki
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A;Status: preliminary; translated from GB/E
A;Molecule type: DNA
A;Residues: 1-409 <FAV>
A;Cross-references: UNIPARC:UPI000017B744;
A;Cross-references: Strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C06E8.3 - Cac
;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_rev.
C;Accession: T15435
R;Favello, A.
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A;Gene: CESP:C06E8
A;Introns: 24/1; 7
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                  RGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG
TGEVKLVDFGATAYAEKATKKEFQGTRSYCPPEWFRDQLYLPLEATSWSLGVLLFILLTG
                                                                                                                          GQQPVAVKFVQHKHVRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV
                                                                                                                                                         -NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLI
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                                                              MERPANCMDLFDMVSVHGPLNEDMGKF1FKQV1TTVFNMYSKHGLLHRD1KDENLIVNMN
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protein kinase
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Pred. No. 6.5e-18;
4; Mismatches 124;
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No. 6.
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A; Experimental s
C; Function:
A; Description: C
C; Superfamily: S
                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                        submitted to the EMBL Data Library, December A;Reference number: Z17020 A;Accession: T10449
                                                                                                                                                                                                probable serine/threonine-specific protein kinase NyAlternate names: SNF1-related protein kinase C;Species: Cucumis sativus (cucumber) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed A;Reference number: 149071; MUID:95200798; PMID:7893599
A;Accession: 149072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: 149072
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149072
                                                                           A; Molecule type: mRNA
A; Residues: 1-504 < GUM>
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                                                              A;Cross-references: UNIPROT:P93113; UNIPARC:UPI00000A4B92; EMBL:Y10036
                                                                                                         A; Status: preliminary; translated
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                                                                                                                                                                                    Accession: T10449;
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catalyzes the formation of peptidyl-serine-phosphate SNF1-related protein kinase; protein kinase homology
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Pred. No. 2e-12;
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A; Reference number: S66723
A; Accession: S66730
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hypothetical protein YOL045w -
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A; Residues: 1-1101 < ANS >
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N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
C;Accession: S66730
R;Anborge, W.; Benes, V.; Rechmann O. Callerian Communication 
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                                                                                                                        SSECOHLIKWCLSLRPSDRPSFEEIRNHPWMQ 291
                                                                                                                                                                                                                                                             VĠŢMDYAAPEVLGGSSYKĠKPQDIWALĠVĹĹŸŢŢŢYKENPYYNIDETLEGELRFDKSEHV
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33.5%; Pred. No. 1.6e-11;
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Pred. No. 8.3e-12;
7; Mismatches 108;
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atabase, July 1996
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C;Genetics:
A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 1
C;Function:
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A; Residues: 144-198 < TH2>
A; Cross-references: UNIPARC: UPI000009DEE0;
A; Cross-references: UNIPARC: UPI00009DEE0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, Gene 120, 249-254, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change C;Accession: JC1446; S58266; S66334
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A; Residues: 1-512 < LEG>
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;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
;147,151/Binding site: magnesium (Asn, Asp) #status predicted
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Best Local
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RDLIPRMLVVDPMKRVTIPEIRQHPWFQAHL
                                                                                                                                                                                                                                                                    ILRLFMHPH--IIRLYEVIETPTDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI
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                                          QHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL
                                                                                       EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPGA
                                                                                                                                    EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI--
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Pred. No. 1.6e-
47; Mismatches
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RESULT 11

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A;Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-864,867-1358 <OUE>
A;Cross-references: UNIPARC:UPI000052EA6; EMBL:L05146; NID:g171851; PIDN:AAC04940.1;
A;Cross-references: UNIPARC:UPI0000052EA6; EMBL:L05146; NID:g171851; PIDN:AAC04940.1;
A;Cross-references: UNIPARC:UPI000052EA6; EMBL:L05146; NID:g171851; Values:UPI000052EA6; Values:UPI000052EA6; EMBL:L05146; NID:g171851; Values:UPI000052EA6; Values:UPI0000052EA6; Values:UPI0000052EA6; Values:UPI0000052EA6; Values:UPI0000052EA6; Values:UPI0
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A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
A;Cross-references: Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisias A;Reference number: S36711
A;Accession: S36711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138 C;Speciles: Saccharomyces cerevisiae C;Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 05-Oct-2004 C;Accession: S33653; S36717; S36732; JH0486 R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton Yeast 9, 543-549, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
S33653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13741
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z17668
A;Reference number: Z17668
A;Accession: T13741
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A;Introns: 205/3; 227/1; 322/3; 688/3;
A;Note: EG:22E5.8
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A;Molecule type: DNA
A;Residues: 1-1398 <MUR>
                          A; Title: Identification of a Saccharomyces A; Reference number: S22266; MUID:92221690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: The YAL017 gene on the left arm of chromosome I A; Reference number: S33653; MUID:93311122; PMID:8322517
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C;Genetics:
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No. 3
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PMID:1561836
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A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonix (;Superfamily: SNF1-related protein kinase; protein kinase homology C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase;17-271/Domain: protein kinase homology <KIN> F;25-33/Region: protein kinase ATP-binding motif F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                  serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - C;Species: Nicotiana tabacum (common tobacco) C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_char C;Accession: A56009 R;Muranaka, T.; Banno, H.; Machida, Y.
                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; UNIPARC:UPI00000AAD0C; GB:D26602;
C;Function:
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A; Reference number: A56009; MUID:94217693; PMID:8164654
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A;Residues: 1-72, E',74-154 <SID>
A;Crose-references: UNIPARC:UPI000017A44B
C;Genetics:
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Gene 107, 111-118, 1991
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A;Molecule type: DNA
A;Residues: 1-862 <CL2>
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A; Map position: 1L
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Matches 88
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)l. Cell. Biol. 14, 2958-2965, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RCVPKRPTIDDINNDKWL
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Pred. No. 4.2e-11;
4; Mismatches 100;
  Score 370;
  DB 1;
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Length 511;
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A;Molecule type: mRNÁ
A;Residues: 1-512 <BHA>
A;Cross-references: UNIPROT:P92958; UNIPARC:UPI00000AC16D;
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999

A;Title: Regulatory interaction of PRLI WD protein with Arabidopsis SNF1-like A;Reference number: Z25116; MUID:99238528; PMID:10220464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis N;Alternate names: SNF1 protein kinase omolog AKIN11 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 05-Oct-2004 C;Accession: T52633
                                                                                                                                                             á
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: EC 2.7.1.-; serine/threonine-specific protein kicomplements SNF1 mutations in yeast C;Superfamily: SNF1-related protein kinase; protein kinase home C;Keywords: ATP; phosphotransferase; serine/threonine-specific
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C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                     92 LLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQV 151
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                                                                                                                                                                      LEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GTRVYSPP
                                                                                                                                                                                                                                                                                                                                     EPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEVVLLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGF 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP
    QHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL
                                             EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSEA
                                                                                    EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI----IKGQVF-FRQTVSSEC
                                                                                                                             ISGVEYCHRNMVVHRDLKPENLLLD-SRCNIKIADFGLSNVMRDGHFLKTSCGSPNYAAP
                                                                                                                                                                                                              ILRLFMHPH--IIRQYEVIETTSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQI
                                                                                                                                                                                                                                                                                              ESILPNYKLGKTLGIGSFGKVKIAEHVVTGHKVAIKILNRRKIKN---MEMEEKVRREIK
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Pred. No.
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9; Mismatches
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C;Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: SNF1-related protein kinase; protein kinase homology C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase F;15-272/Domain: protein kinase homology <KIN> F;23-31/Region: protein kinase ATP-binding motif F;23-31/Region: protein kinase ATP-binding motif F;46,65,143,145/Active site: Lys, Glu, Asp, Lys #status predicted F;148,152/Binding site: magnesium (Asn, Asp) #status predicted
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submitted to the EMBL Data Library, April 1992
A;Recension: S24578
A;Recession: S24579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Halford, N.G.; Vicente-Carbajosa, J.; Sabelli, P.A.; Shewry, P.R.; Hannappel, U.; Krei Plant J. 2, 791-797, 1992
A;Title: Molecular analyses of a barley multigene family homologous to the yeast proteir A;Reference number: S60303; MUID:93258420; PMID:1302632
A;Accession: S60304
Search completed: May 4, 2006, 05:25:51 Job time: 21.3333 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-61'A',63-513 <HA2>
A;Cross-references: UNIPARC:UPI00000A3F6F; EMBL:X65604; NID:gl8933; PIDN:CAA46554.1; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-513 <HALD
A;Cross-references: UNIPROT:Q40030; UNIPARC:UPI000017255D; EMBL:X65604
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S60304
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;Date: 19-Mar-1997 #sequence_revision 15-Aug-1997 #text_change 05-Oct-2004
;Accession: S60304; S24579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Local Similarity 34.1%;
hes 94; Conservative 4
                                                                                                              241
                                                                                                                                                                                                                                                                          205
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                                                                                                                                                                                                                     181 LNYAAPETISSKLYAGPEVDVWSCGVVLYALLCGSVPFDDDNIPSLFRKIKGGTYILPSY 240
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                                                                                                                                                VSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
                                                                                                                                                                                                                                                                  RVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDE----EIIKGQVFFRQT-
                                                                                                                                                                                                                                                                                                                        RIFQQILAGVEYCHRIMVVHRDLKPENLLLD-SRYNVKLADFGLSNVMRDGHFLKTSCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEVVLLKKVSSDF--SGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLAR 145
                                                                                                         LSDSARDLIPKLLNIDPMKRITFHEIRVHPWFKNHL
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PIR; A24169; TVMSP1.
HSSP; Q63450; 1A06.
SMR; P06803; 32-308.
Ensembl; ENSMUSG0000024014; Mus musculus.
MGI; MGI: 97584; Piml.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR00071; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
ProDom; PD000001; Prot_kinase; 1.

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RC STRAIN-C57BL/6; TISSUE-Brain, and Eye;

RC MEDLINE-C2388257; pubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Garcuse L.H., Derge J.G.,

RI Alusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., NcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation updat
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PROSITE; PS00101; PROTEIN_KINASE_DM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
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PRODOM; PD000001; Prot kinase; I.

SMART; SM00220; S_TKC; I.

PROSITE; PS00107; PROTEIN KINASE ATP; I.

R PROSITE; PS50011; PROTEIN KINASE DOM; I.

R PROSITE; PS00108; PROTEIN KINASE ST; I.

R PROSITE; PS00108; PROTEIN KINASE ST; I.

W ATP-binding; Kinase; Nucleotide-binding;

W Serine/threonine-protein kinase; Transferase.

W Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUDI-2003) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; BC022885; AAH42885.1; -; mRNA.

EMBL; BC053019; AAH53019.1; -; mRNA.

EMBL; BC055316; AAH55316.1; -; mRNA.

SMR; OBCFN8; 32-308.

Ensembl; ENSMUSCOOOF
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:Protein serine/threonine kinase activity;
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR000871; Ser_thr_pkin_AS.
InterPro; IPR008271; Ser_thr_pkin_ase.
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Submitted (JUN-2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6; TISSUE=Brain;
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                         EIHLHSLSPGSSK
                                                                  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS
                                                                                                          EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
                                                                                                                       EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI
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l. Acad. Sci. U.S.A. 99:16899-16903(2002)
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ProDom; PD000001; Prot kinase; 1.

PROSITE; PS00101; PROTEIN KINASE ATP; 1

PROSITE; PS50011; PROTEIN KINASE DOM; 1

PROSITE; PS00108; PROTEIN KINASE ST; 1.
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Q95LJ0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felida
Felinae; Felis.
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SMR; Q95LJ0; 32-308.
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InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Ser_thr_pkin_AS.
InterPro; IPR0008271; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_ST; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding; PROFERM; RINASE ST; 1.
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"Characterization of the testes-specific pim-1 tra
Nucleic Acids Res. 20:3183-3189(1992).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a
-!- SUBUNIT: Binds to RP9 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear
-!- PTW: Autophosphorylated (By similarity).
-!- SIMILARITY: Belongs to the Ser/Thr protein kin
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
Name=Piml, Synonyms=Pim-1;
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalia; Butheria; Buarchontoglires; Glires;
Muroidea; Muridae; Murinae; Rattus.
MCBI_TaxID=10116;
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NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Stausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.I.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.
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P11309; O96RG3;
01-JUL-1989 (Rel. 11, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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Zakut-Houri R., Hazum S., Gi
"The CDNA sequence and gene
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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"Cloning and characterization of the human
oncogene related to the protein kinases.";
J. Cell. Biochem. 35:105-112(1987).
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azum S., Givol D., Telerman A.;
e and gene analysis of the human pim oncogene.";
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Barr P.J., Power M.;
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EMBL; M27903; AAA60090.1; -; Genomic EMBL; M16750; AAA60089.1; -; MRNA. EMBL; M54915; AAA36447.1; -; mRNA. EMBL; M24779; AAA36453.1; -; mRNA. EMBL; M24779; AAA81553.1; -; mRNA. EMBL; BC020224; AAH70224.1; -; mRNA. EMBL; AF386792; AAK70871.1; -; Genom: PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; TVHUP1. PIR; JU0337; AP14-313. PDB; 1XR1; X-ray; A=14-313. PDB; 1XR1; X-ray; A=1313. PDB; 1XHS; X-ray; A=33-305.
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[7]
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MEDLINE=21354098; PubMeda11460166; DOI=10.1038/35085588;

Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,

Chaganti R.S.K., Kuppers R., Dalla-Favera R.;

"Hypermutation of multiple proto-oncogenes in B-cell difficell lymphomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4; Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.; "Identification of heterochromatin protein 1 (HP1) as a phosphorylation target by Pim-1 kinase and the effect of phosphorylation on the transcriptional repression function of HP1."; FEBS Lett. 467:17-21(2000).
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"Identification of the human pim-1 gene product as a
cytoplasmic protein with tyrosine kinase activity.";
Mol. Cell. Biol. 8:1498-1503(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22567470; PubMed=12680209;
IONOV Y., Le X., Tunquist B.J., Sweetenham J.,
Johnson T., Lilly M.B., Kraft A.S.;
"Pim-1 protein kinase is nuclear in Burkitt's
localization is necessary for its biologic eff
Anticancer Res. 23:167-178(2003)
-!- FUNCTION: Thought to play a role in signal
cells. May affect the structure or silenci
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proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                   This
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MEDLINE=88246418;
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                                                                                                                                                                                                                                                                                                                                                                                                            phosphoryiating HP1 gamma/CBX3.

CATALTYIC ACTIVITY: ATP + a protein = ADP + a SUBUNIT: Binds to RP9 (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic and nuclear. TISSUE SPECIFICITY: Expressed primarily in celhematopoietic and germ line lineages.

PTM: Autophosphorylated on tyrosine residues.

SIMILARITY: Belongs to the Ser/Thr protein kin
                                                                                                                                                                                                                                                                    s Swiss-Prot entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the ENEUROPEAN BIOINFORMATICS Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                          subfamily.
DATABASE: 1
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WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIM1ID261.html".
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PDB; 1Y14; X-ray; A=33-05.
PDB; 2B1K; X-ray; B=1-313.
PDB; 2B1L; X-ray; B=1-313.
Ensembl; ENSG00000137193; Homo s
HGNC; HGNC:8986; PIM1.
H-InvDB; HIX0005835; -...
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H7 HUMAN
H7 HUMAN PRELIMINARY; PRT; 313 AA.
Q5TTH7; HUMAN PRELIMINARY; PRT; 313 AA.
Q5TTH7;
Q1-FEB-2005 (TrEMBLrel. 29, Created)
Q1-FEB-2005 (TrEMBLrel. 29, Last sequence update)
Q1-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Pim-1 oncogene (Proviral integration site 1).
Name=PIM1; ORFNames=RP3-355M6.1-003;
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CONFLICT
SEQUENCE
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G0; G0:0005737; C:cytoplasm; TAS.
G0; G0:0004674; F:protein serine/threonine kinase activity;
G0; G0:0004674; F:protein serine/threonine kinase activity;
G0; G0:0007275; P:development; TAS.
G0; G0:0006469; P:protein amino acid phosphorylation; TAS.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_Ehr_pkin_AS.
PF4am; PF00069; Pkinase; I.
  Homo.
NCBI_TaxID=9606,
[1]
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PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
                                                                     Mammalia;
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Eukaryota; Metazoa; (
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44
167
67
15
313 /
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35686
                                                                Euarchontoglires;
                                                                                       Chordata;
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93
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ATP (By similarity).

Proton acceptor (By s

ATP (By similarity).
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Pred. No. 5
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                                                                Craniata; Vertebra
oglires; Primates;
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                                                                                       Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .le-109;
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                                                                   Catarrhini;
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                                                                                       Euteleostomi;
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RESULT 7
PIM1_BOVIN
ID PIM1_B
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Best Local S
Matches 294
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R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004674; F:protein serine/threonine kinase activit
R GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
R GO; GO:0004713; F:protein amino acid phosphorylation; IEA.
R GO; GO:000468; P:protein amino acid phosphorylation; IEA.
R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
R InterPro; IPR000271; P:protein amino acid phosphorylation; IEA.
R InterPro; IPR002290; Ser_thr_pkin_AS.
R InterPro; IPR002290; Ser_thr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR0012745; Tyr_pkinase.
R FAmn; PR00069; Pkinase; I.
R SMART; SM00210; TyrKC; 1.
R SMART; SM00210; TyrKC; 1.
R SMART; SM00210; TyrKC; 1.
R PROSITE; PS0011; PROTEIN_KINASE_ATP; 1.
R PROSITE; PS00101; PROTEIN_KINASE_BT; 1.
R PROSITE; PS00101; PROTEIN_KINASE_ST; 1.
                                                                                                             Bos taurus (Bovine).

Bukaryota, Metazoa; Chorda
Mammalia; Eutheria; Lauras.

Pecora; Bovidae; Bovinae; i

NCBI TaxID=9913;
                                                                                                                                                                                                                                                                                                                                      Q9N0P9;
28-FEB-2003
28-FEB-2003
13-SEP-2005
NUCLEOTIDE SEQUENCE.
MEDLINE=21109090; PubMed=11182156;
Wang Z., Petersen K., Weaver M.S.,
                                                                                                                                                                                                                                                                                    Name=PIM1;
                                                                                                                                                                                                                                                                                                             Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL353579; CAIZ
SMR; Q5T7H7; 32-308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOVIN
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||||||||:||||||||||||:
PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA
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(Rel. 41,
(Rel. 48,
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el. 48, Last annotation update)
serine/threonine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPGPSK
                                                                                                                                                                                         Chordata; Crani
Laurasiatheria;
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93.9%;
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Pred. No. 5.1e
LO; Mismatches
                                                                                                                                                                                         Craniata; Vertebrata;
heria; Cetartiodactyla;
         DOI=10.1016/S0165-2427(00)00259-2; Magnuson N.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313
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les 9;
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                                                                                                                                                                                         Euteleostomi; Ruminantia;
                                                                                                                                                                                                                                                                                                             (E)
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RESULT 8
PIM3_COTJA STANDARD; PRT; 323 AA.
ID PIM3_COTJA STANDARD; PRT; 323 AA.
AC Q9PUB5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2005 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)
GN Name=PIM3; Synonyms=PIM-3;
GS Coturnix coturnix japonica (Japanese quail).
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InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
ProDom; PD000001; Prot_kinase; 1.
ProDom; PD000001; Prot_Kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding; Phosphorylation; Proto-oncogene; Serine/threonine-protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMR; Q9N0P9; 32-308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NA cloning, sequencing and characterization of Immunol. Immunopathol. 78:177-195(2001).

CATALYTIC ACTIVITY: ATP + a protein = ADP + a | SUBUNIT: Binds to RP9 (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic and nuclear PTM: Autophosphorylated (By similarity).

SIMILARITY: Belongs to the Ser/Thr protein kin.
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292; Conserv
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Pred. No. 2e-1
L2; Mismatches
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ATP (By similarity).
Proton acceptor (By similarity).
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ATP (By similarity).
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NUCLEOTIDE SEQUENCE.

MEDLINE=20180111; Pubmed=10713710; DOI=10.1038/sj.onc.1203355;

Bichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;

"Developmental expression of Pim kinases suggests functions also outside of the hematopoietic system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKG; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
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-!- CATALYTIC ACTIVITY: ATP + a protein
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Coturnix.
NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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InterPro; IPR008271; Ser thr pkin As.
InterPro; IPR002290; Ser thr pkinase.
Pfam; PF00069; Pkinase; I.
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HSSP; Q63450; 1
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                                                                                                            DIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWM-QGDLLPQ
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                                       AASEIHLHSL
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                                                                                                                                                                                                                                                                     VMERPELVKDLFDFITEKGALDEDTARGFFRQVLEAVRHCYGCGVVHRDIKDENLLVDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                               MLLSKFGSLAHICSPASMDHLPVKILPPVKVEKEPFDKVYQVGSVLGSGGFGTVYAGSRT
EDCDIRLRTL
                                                                                   DIPFEQUEEILRGRLYFRRRISPECQQLIKWCLSLRPSDRPTLEQIFDHQWMHKSEVVKS
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168
69
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67.1%;
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Pred. No. 1.
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Proton acceptor (By Bimilarity).
ATP (By similarity).
ATP (By similarity).
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1.3e-75;
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STANDARD;

326

28-FEB-2003 28-FEB-2003 13-SEP-2005

(Rel. (Rel.

41, Created)
41, Last sequence update)
48, Last annotation updat
protein kinase Pim-3 (EC 2

update) (EC 2.7.1.37)

δ В Ş S 밁 Š 밁

В

Mus musculus (Mouse)

Name=Pim3

Serine/threonine-protein

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=TUB/N; TISSUE=COOlon, and Salivary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242600; MEDLINE, Schuetr G.D., Bat N.K., RA Hopkins R.F., Jordan H., May S.J., Hong L., Schect T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Richards S., McGrean P.J., Malek J.A., Gunaratne P.H.,

RA Richards S., McGrean R.J., Malek J.A., Gunaratne P.H.,

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RA Rodriguez A.C., Grimwood J., Schewtz J., Myers R.M.,

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RA Rodriguez A.C., Grimwood J., Schewtz J.M., Marra M.A.;

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RA Rodriguez A.C., Grimwood J., Schewtz J.M., Marra M.A.;

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RA Rodriguez A.C., Grimwood J., Schewtz B.,

RA Rodriguez A.C., Grimwood J., Schewtz B.,

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Best Local Similarity
Matches 213; Conserv
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DOMAIN 40 293

NP BIND 46 54

ACT SITE 170 170

BINDING 69 69

SEQUENCE 326 AA; 35970 M
                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Nuclectide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI; MGI:1355297; Pim3: MUSK MUSK INTERPROPERTY PRODUCTS; PROBERT; Ser_thr_pkin_AS. InterPro; IPRO08271; Ser_thr_pkin_AS. InterPro; IPRO02290; Ser_thr_pkinase. Pfam; PP00069; Pkinase; I.
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EMBL; BC026639; AAH26639.1; -;
HSSP; Q03656; 1HOW
Ensembl; ENSMUSG00000035828; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use as
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Mammalia; E
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Euarchontoglires; Glires; Rodentia; Sciurognathi;
Murinae; Mus.
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ATP (By similarity).
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31; Mismatches
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               EMBL; AF086624; AAC68900.1; ALT_INIT; mRNA.

EMBL; AF057026; AAC38065.1; -; mRNA.

RSSP; QO3656; 1HOW.

RGD; 620462; Pim3.

GO; GO:00046774; F:protein serine/threonine kinase aci
GO; GO:00046777; P:autophosphorylation; IDA.
GO; GO:0016572; P:histone phosphorylation; IDA.
InterPro; IPR00719; Prot kinase.

InterPro; IPR008271; Ser_thr_pkin_AS.

InterPro; IPR002290; Ser_thr_pkin_AS.

Pfam; PP00069; Pkinase; I.

PFCDOM: DD000001. Bort three. 1
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Submitted
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-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a protein = TISSUB SPECIFICITY: Present in a number of unst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley;
Konietzko U., Kuhl D.;
"Pim-3 is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         070444;
28-FEB-2003
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13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase pim-3 (EC 2.7.1.37)
Kid-1) (Kinase induced by depolarization).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Euarchonto
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28-FEB-2003 (Rel. 41,
13-SEP-2005 (Rel. 48,
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INDUCTION: By membrane depolarization
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Vician L., Crispino M., Tocco G., Marcheselli V.L
Waudry M., Herschman H.R.;
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Bioinformatics and the EMBL
titute. There are no restrict
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Rodentia; Sciurognathi;
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                                                                                                                                                                           activity;
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MBL outstation -
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             REDIINE-22388357, bubmed=12477932; DOI=10.1073/pnas.242603899;

X MEDIINE-22388357, bubmed=12477932; DOI=10.1073/pnas.242603899;

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Logleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Stapleton M., Gudin T.B., Toshiyuki S., Carninci P., Prange C.,

X Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

X Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Bosak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,

X Bosak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,

X Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,

X Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,

X Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,

X Blakesley R.W., Touchman J.W., Green E.D., Muzna M.A.,

X Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 213
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M2 RAT

Q4V8M2 RAT

Q4V8M2;

13-SEP-2005

13-SEP-2005

13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-yep-2005 (Tremblrel.)
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Muroidea; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVVHRDIKDEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWEER
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 CDNA
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
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71.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1122.5; DB 1; Length Pred. No. 5.7e-75;
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ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 213
                                                          TISSUE=Liver;
PubMed=15540201; DOI=10.1002/ijc.20719;
Puisi C.. Nakamoto Y., Lu P., Tsuneyama
                                                                                                                                                                                                                 PIM3_HUMAN STANDARD; PRT; 326 AP
Q86V86; Q68BM2;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine/threonine-protein kinase; Transferase.
NON_TER 1 1 1
SEQUENCE 380 AA; 41568 MW; F82BE8E50DD713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRODOM; PD000001; Prot_kinase; 1.
SMART; SM00220; STK; 1.
SMART; SM00219; TYCK; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Hypothetical_protein; Kinase; Nucleotide-binding;
           Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova Kaneko S., Mukaida N.;
"Aberrant expression of serine/threonine kinase Pim-3 hepatocellular carcinoma development and its role in tof human hepatoma cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                 Homo.
                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; Pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: Belongs to the Ser/Thr protein kinase fambL; BC097317; AAH97317.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
                                                                                                      NUCLEOTIDE SEQUENCE [MRNA], FUNCTION,
                                                                                                                                   NCBI_TaxID=9606
                                                                                                                                                               Mammalia;
                                                                                                                                                                                                         Name=PIM3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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213; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
                                                                                                                                                                                                                                                                                                                                                         YDMVCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWMLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000719; Prot kinase.
IPR008271; Ser thr pkin AS.
IPR002290; Ser thr pkinase.
IPR001245; Tyr pkinase.
                                                                                                                                                              ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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71.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1122.5;
Pred. No. 6.9e.
31; Mismatches
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                                                                                                          AND
                                                                                                                                                                                                                    update)
(EC 2.7.1.37).
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                                                                 Popivanova B
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                                                                                                          SPECIFICITY
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                            the
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Raha S.S., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Raha S.S.N., Kzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human
"T and mouse CNMA sentences":
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SEQUENCE 326 AA; 35863 M
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MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6; Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.; "Consistency checks for characterizing protein forms."; "Consult Biol. Chem. 27:29-35(2003).

-!- FUNCTION: May be involved in cell cycle progression and antiapoptosis process. Implicated in proliferation of human hepatoma
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
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Ensembl; ENSG00000198355;
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ProDom; PD000001; Prot_kinase;
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InterPro; IPR008271; Ser_thr_pkin_AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. TISSUE SPECIFICITY: Widely expressed. No expression in colon, thymus, and small intestine. Expressed in human hepatoma cell lines but not in normal liver tissues.

SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                            Similarity
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InterPro; IPR00871; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; I.r_pkin_AS.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vej
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine/threonine-protein kinase Pim-3 Name=PIM3; Synonyms=PIM1; Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L29495; AAA85389.1; -; mRNA.
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                                                                                                                                             Serine/threonine-protein
DOMAIN 40 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification of the autophosphorylation im-1 proto-oncogene-encoded protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3iol. Chem. 272:10514-10521(1997).
CATALYTIC ACTIVITY: ATP + a protein = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: Was originally (Ref.1) called Pim-1 but
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                                                                        ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
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; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Xenopus laevis
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RESULT 14
QB11XB MOUSE
ID 11XB MOUSE
AC QB11XB;
DT 01-JUN-2003 (T
DT 01-JUN-2003 (T
DT 01-MAR-2004 (T
DT 01-MAR-2004 (T
DG Name=Pim3; Syn
OS Mus musculus (
OC Eukaryota; Met
OC Muridae; Murin
OX NCBI_TaxID=100
RN [1]
RP NUCLEOTIDE SEC
RA YU L.;
RP NUCLEOTIDE SEC
RA YU L.;
SUBMILTED (JAN
CC -!- SIMILARTIY
DR SMR; QB11XB; 3
DR MGI; MGI:13552
DR HSSP; Q03656;
DR SMR; QB11XB; 3
DR GG; GO:0004674
DR GG; GO:0004674
DR GG; GO:000695
DR InterPro; IPRC
DR InterPro; IPRC
DR InterPro; IPRC
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DR PROSITE; PSOO1
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Best Local S
Matches 212
                                                     Query Match
Best Local S
Matches 208
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                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                 Name=Pim3; Synonyms=Kid1; Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                               Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
 Local Similarity
hes 212; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297
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                                            35931 MW;
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            66.5%;
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26,
                                    kinase; Transieruu.
A MW; 77DEF8E20F41E3F4
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 32;
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Last sequence up
Last annotation
Score 1110; DB 2;
Pred. No. 4.8e-74;
2; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1113;
Pred. No. 2
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AB4DD61E7A99A38F CRC64;
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RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Massant T.L., Scheet T.E.,

RA Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generstion and initial analysis of more than 15 0.00 full-length human

"Generstion and initial analysis of more than 15 0.00 full-length human

"Generstion and initial analysis of more than 15 0.00 full-length human
Klein S., Gerhard D.S.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BC081340; AAH81340.1; -; mRNA.
SMR; O66111; 32-297.
Ensembl; ENSXETG000000009354; Xenopus tropicalis.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus tropicalis (Western clawed frog) (Silurana tropicalis), Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopos; Silurana.
                                                                                                                                                                                                                                                                                                                             "Generation and initial analysis and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233
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DR InterPro; IPR008271; Ser_thr_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

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